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99577

From: Saidha, Tekchand  
Sent: Thursday, July 24, 2003 10:35 AM  
To: STIC-Biotech/ChemLib  
Subject: 09/663481

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(STIC)

**09/663481**

Please search the data bases and interference files for \_

SEQ ID NO : 1 and

SEQ ID NO : 2

Thank you !

*Tekchand Saidha*  
*Primary Examiner*  
*Art Unit 1652, CM1, Room No. 10D05*  
*Mail Box 10D01*  
*(703) 305-6595*

Searcher: M. Smith  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 7/30 - 8/1/03  
Searcher Prep/Review: 4  
Clerical: 5  
Online time: 10

TYPE OF SEARCH:  
NA Sequences: 1  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 10, 2003, 22:28:01 ; Search time 73 Seconds  
(without alignments)  
1121.958 Million cell updates/sec

Title: US-09-663-481-1  
Perfect score: 2676  
Sequence: 1 MANFPVPVQRSHQGLTLRLR.....EEAPPSPAEDHNQNGNLD 516

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
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23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2676	100.0	516	22 AAB35470	Human cyclic nucle
2	2582	96.5	536	20 AAW95110	Human RPMI 8392 ce
3	2484.5	92.8	534	16 AARG9720	Cyclic-GMP stimula
4	2484.5	92.8	534	18 AAW18038	Bovine brain 63 kD
5	2484.5	92.8	534	18 AAW11251	63 kD calcium/cal
6	2484.5	92.8	534	19 AAW77039	Bovine brain Ca2+/
7	2484.5	92.8	534	19 AAW71223	63 kDa Cam-PDE enc
8	2484.5	92.8	534	19 AAW60751	63 kDa bovine Cam-
9	2484.5	92.8	534	21 AAY80977	Bovine brain 63 kD

10	2484.5	92.8	534	24 AAB58716	Bovine brain 63kDa
11	2478.5	92.6	534	13 AAR28404	63 kD Cam PDE from
12	1636.5	61.2	514	16 AAR69715	Cyclic-GMP stimula
13	1636.5	61.2	514	18 AAW18037	Bovine lung 59 kDa
14	1636.5	61.2	514	18 AAW11240	Calcium/calmodulin
15	1636.5	61.2	514	19 AAW77037	Bovine lung Ca2+/c
16	1636.5	61.2	514	19 AAW71221	59 kDa Cam-PDE fro
17	1636.5	61.2	514	19 AAW60749	59 kDa bovine Cam-
18	1636.5	61.2	514	21 AAY80972	Bovine lung 59 kD
19	1636.5	61.2	514	24 AAB58711	Bovine heart full
20	1633.5	61.0	514	13 AAR28401	Bovine lung 59 kD
21	1593	59.5	634	16 AAR69732	Cyclic-GMP stimula
22	1593	59.5	634	18 AAW18040	Human brain 61 kDa
23	1593	59.5	634	18 AAW11256	Hippocampus calcu
24	1593	59.5	634	19 AAW71228	Human 61 kDa Cam-p
25	1593	59.5	634	19 AAW77044	Ca2+/calmodulin st
26	1593	59.5	634	19 AAW60756	Amino acid sequenc
27	1593	59.5	634	21 AAY80989	Human 61 kD Cam-PD
28	1593	59.5	634	24 AAB58728	Cyclic-GMP stimula
29	1591.5	59.5	530	16 AAR69711	Bovine brain 61 kD
30	1591.5	59.5	530	18 AAW18036	Bovine brain 61 kD
31	1591.5	59.5	530	18 AAW11243	Bovine brain Ca2+/
32	1591.5	59.5	530	19 AAW77036	61 kDa Cam-PDE DNA
33	1591.5	59.5	530	19 AAW71220	61 kDa bovine Cam-
34	1591.5	59.5	530	19 AAW60747	Bovine brain 61 kD
35	1591.5	59.5	530	21 AAY80968	Bovine brain full
36	1591.5	59.5	530	24 AAB58707	Bovine brain Cam P
37	1589.5	59.4	530	13 AAR28395	Prod. cDNA insert
38	1576	58.9	634	13 AAR28412	Cyclic-GMP stimula
39	1568.5	58.6	535	16 AAR69731	Human brain 61 kDa
40	1568.5	58.6	535	18 AAW18039	Hippocampus calcu
41	1568.5	58.6	535	18 AAW11255	Human 61 kDa Cam-p
42	1568.5	58.6	535	19 AAW71227	Human Ca2+/calmodu
43	1568.5	58.6	535	19 AAW77043	Amino acid sequenc
44	1568.5	58.6	535	19 AAW60755	Human 61 kD Cam-PD
45	1568.5	58.6	535	21 AAY80988	

ALIGNMENTS

RESULT 1

AAB35470  
ID AAB35470 standard; protein; 516 AA.

XX AAB35470;

AC AAB35470;

XX 06-JUN-2001 (first entry)

XX Human cyclic nucleic acid phosphodiesterase PDE1B2.

XX Human; cyclic nucleic acid phosphodiesterase; PDE1B2; spleen;  
XX cardiovascular disease; gastrointestinal disorder; sexual dysfunction.

XX Homo sapiens.

XX EPI085092-A1.

XX 21-MAR-2001.

XX 14-SEP-2000; 2000EP-0307982.

XX 17-SEP-1999; 99GB-0022125.

XX (PFIZ ) PFIZER LTD.

XX (PFIZ ) PFIZER INC.

XX Fidoock MD;

XX WPI; 2001-246901/26.

XX N-PSDB; AAF62301.

XX Human cyclic nucleotide phosphodiesterase 1B2 and its nucleotide

PT sequence useful for treating cardiovascular, gastrointestinal and  
 PT spleen disorders and screening for drugs to treat associated disorders

XX Claim 1; Page 42-45; 58pp; English.

XX The present invention provides the protein and coding sequences for the  
 CC human cyclic nucleic acid phosphodiesterase PDE1B2. This is thought to be  
 CC a splice variant of PDE1, and capable of catalyzing the degradation of  
 CC cAMP and/or cGMP. The sequences are useful in the treatment of  
 CC cardiovascular, gastrointestinal and spleen disorders, and in the  
 CC enhancement of the male erectile response and treatment of female sexual  
 CC dysfunction. The present sequence is the PDE1B2 protein.

XX Sequence 516 AA;

Query Match 100.0%; Score 2676; DB 22; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-245;  
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANPVPQVSHLOGPILRLRYMVKOLENGEINTEELKKNLEYTASLLEAVYIDETQIIL 60

DB 1 MANPVPQVSHLOGPILRLRYMVKOLENGEINTEELKKNLEYTASLLEAVYIDETQIIL 60

QY 61 TEDELQELSDAVSEVROWLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFVERMP 120

DB 61 TEDELQELSDAVSEVROWLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFVERMP 120

QY 121 RTTYSVGPYSTAVLNCLNLDWCDFVSLNQAADHALRTIVFELLRHNLSIRFKIP 180

DB 121 RTTYSVGPYSTAVLNCLNLDWCDFVSLNQAADHALRTIVFELLRHNLSIRFKIP 180

QY 181 TVFLMSFLDALETGYKYNPNYHQIHAADVDTQVHCFLRTGMVHCLSEIELLAIFAA 240

DB 181 TVFLMSFLDALETGYKYNPNYHQIHAADVDTQVHCFLRTGMVHCLSEIELLAIFAA 240

QY 241 AIHDYHTGTNSFHQIOTSECAIVYNDRSVLENHHISSVFRMQDDNMNIFNLTKDEF 300

DB 241 AIHDYHTGTNSFHQIOTSECAIVYNDRSVLENHHISSVFRMQDDNMNIFNLTKDEF 300

QY 301 VELRALVIEMLVLTMSCHFFQOQVTKMTALQQLERIDKPKALSLLHAADISHPTKQWLV 360

DB 301 VELRALVIEMLVLTMSCHFFQOQVTKMTALQQLERIDKPKALSLLHAADISHPTKQWLV 360

QY 361 HSRWTKALMBEFPFGDKEAELGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSVLTDVA 420

DB 361 HSRWTKALMBEFPFGDKEAELGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSVLTDVA 420

QY 421 EKSVPQPLADEDSKKNQPSQFWRQPSLDVEVDGPNPDVYSFRSTWVKRIQENKQWKERA 480

DB 421 EKSVPQPLADEDSKKNQPSQFWRQPSLDVEVDGPNPDVYSFRSTWVKRIQENKQWKERA 480

QY 481 ASGITNOMSIDELSPCEEAPPSPAEDHNQNGLD 516

DB 481 ASGITNOMSIDELSPCEEAPPSPAEDHNQNGLD 516

RESULT 2

AAW95110 standard; Protein; 536 AA.

XX AC AAW95110;

XX DT 26-MAY-1999 (first entry)

XX Human RPMI 8392 cell phosphodiesterase, PDE1B1.

XX Antisense oligodeoxynucleotide; phosphodiesterase; PDE1B1; enzyme; PDE;

XX cell death; apoptosis; cancer; Ca2+-calmodulin; lymphoblastoid; RNase H;

XX RPMI 8392; RNA degradation; CAMP; immunoproliferative disorder; breast;

XX Immune dysfunction; acute lympholytic leukemia; prostate; human.

XX Homo sapiens.

OS

XX US585834-A.

XX 23-MAR-1999.

XX 30-SEP-1997.

XX 30-SEP-1996;

XX 30-SEP-1997;

XX (EPST/) EPSTEIN P M.

XX Epstein PM;

XX WPI; 1999-228548/19.

XX N-PSDB; AAX26288.

XX Antisense oligodeoxynucleotides specific for mRNA encoding

XX phosphodiesterase PDE1B1 enzymes and method for using them to induce

XX apoptosis of cells - useful in the treatment of immunoproliferative

XX disorders and immune dysfunctions

XX Disclosure; Fig 8A-D; 35pp; English.

XX The invention relates to antisense oligodeoxynucleotides (AS-ODN) which

XX will bind to mRNA encoding phosphodiesterase PDE1B1 enzymes and their use

XX in inducing programmed cell death (apoptosis) in cancer cells. PDE1 is a

XX Ca2+-calmodulin dependent phosphodiesterase found in cytosolic extracts

XX of human lymphoblastoid cell line, RPMI 8392. The method in which

XX programmed cell death is induced in cancer cells comprises: (1)

XX identifying the phosphodiesterase enzyme PDE1B1 in a cell line containing

XX the cancer cells; (2) synthesizing an AS-ODN inhibitor which will bind to

XX mRNA encoding PDE1B1; and (3) applying the AS-ODN to the cell line to

XX inhibit the enzymatic activity of the PDE1B1 and induce apoptosis in the

XX cells. The AS-ODNs inhibit the expression of a protein by two mechanisms:

XX (i) by degradation of RNA by the ubiquitous enzyme RNase H, which

XX selectively cleaves the RNA of DNA-RNA heteroduplexes; and (ii) the

XX arrest of translation initiation caused by AS-ODN hybridization to the 5'

XX un-translated region or the translation initiation site on the mRNA.

XX Inhibition of phosphodiesterase (PDE) enzyme expression results in

XX elevated levels of cAMP in the cells due to PDE1B1 being involved in the

XX metabolism of cAMP. The elevated cAMP levels result in apoptosis by

XX inhibition of DNA synthesis. The method and AS-ODN are useful in inducing

XX cAMP stimulated apoptosis and in the treatment of immunoproliferative

XX disorders and immune dysfunctions such as acute lympholytic leukemia,

XX breast and prostate cancer. The present sequence represents a human RPMI

XX 8392 cell PDE1B1.

XX Sequence 536 AA;

Query Match 96.5%; Score 2582; DB 20; Length 536;

Best Local Similarity 100.0%; Pred. No. 6.5e-236;

Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LRYVVKOLENGEINTEELKKNLEYTASLLEAVYIDETQIILTEDELQELSDAVSEVR 78

DB 19 LRYVVKOLENGEINTEELKKNLEYTASLLEAVYIDETQIILTEDELQELSDAVSEVR 78

QY 39 LRYVVKOLENGEINTEELKKNLEYTASLLEAVYIDETQIILTEDELQELSDAVSEVR 98

DB 39 LRYVVKOLENGEINTEELKKNLEYTASLLEAVYIDETQIILTEDELQELSDAVSEVR 98

QY 79 DMLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFVERMPRTTYSVGPYSTAVLNCL 138

DB 79 DMLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFVERMPRTTYSVGPYSTAVLNCL 138

QY 99 DMLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFVERMPRTTYSVGPYSTAVLNCL 158

DB 99 DMLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFVERMPRTTYSVGPYSTAVLNCL 158

QY 139 KNLDLWCDFVSLNQAADHALRTIVFELLRHNLSIRFKIPFTVFLMSFLDALETGYGKY 198

DB 139 KNLDLWCDFVSLNQAADHALRTIVFELLRHNLSIRFKIPFTVFLMSFLDALETGYGKY 198

QY 159 KNLDLWCDFVSLNQAADHALRTIVFELLRHNLSIRFKIPFTVFLMSFLDALETGYGKY 218

DB 159 KNLDLWCDFVSLNQAADHALRTIVFELLRHNLSIRFKIPFTVFLMSFLDALETGYGKY 218

QY 199 KNPYINQIHAADVDTQVHCFLRTGMVHCLSEIELLAIFAAAIHDYHTGTNSFHIQT 258

DB 199 KNPYINQIHAADVDTQVHCFLRTGMVHCLSEIELLAIFAAAIHDYHTGTNSFHIQT 258

QY 219 KNPYINQIHAADVDTQVHCFLRTGMVHCLSEIELLAIFAAAIHDYHTGTNSFHIQT 278

DB 219 KNPYINQIHAADVDTQVHCFLRTGMVHCLSEIELLAIFAAAIHDYHTGTNSFHIQT 278

QY 259 KSECAIVYNDRSVLENHHISSVFRMQDDNMNIFNLTKDEFVLRALVIEMLVLTMSCH 318

DB 259 KSECAIVYNDRSVLENHHISSVFRMQDDNMNIFNLTKDEFVLRALVIEMLVLTMSCH 318

QY 279 KSECAIVYNDRSVLENHHISSVFRMQDDNMNIFNLTKDEFVLRALVIEMLVLTMSCH 338

DB 279 KSECAIVYNDRSVLENHHISSVFRMQDDNMNIFNLTKDEFVLRALVIEMLVLTMSCH 338

QY 319 HFQOVKMTALQQLERIDKPKALLSLLHAADISHTPKQWLHVRWTKALMEEFPRQGD 378  
DB 339 HFQOVKMTALQQLERIDKPKALLSLLHAADISHTPKQWLHVRWTKALMEEFPRQGD 398  
QY 379 EAEGLPFPPLCDRTSTLVAQSIQIGFIDIVEPTFSLTDVAEKSVQPLADESKSNOP 438  
DB 399 EAEGLPFPPLCDRTSTLVAQSIQIGFIDIVEPTFSLTDVAEKSVQPLADESKSNOP 458  
QY 439 SFQWQPSLDVEGPNPDVFSRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 498  
DB 459 SFQWQPSLDVEGPNPDVFSRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 518  
QY 499 EAPPSPAEDEHNGNGLD 516  
DB 519 EAPPSPAEDEHNGNGLD 536

RESULT 3  
AAR69720  
ID AAR69720 standard; Protein; 534 AA.

XX AAR69720;

XX 25-MAR-2003 (updated)

DT 11-OCT-1995 (first entry)

XX Cyclic-GMP stimulated nucleotide PDE clone p12-3a.

DE Cyclic-GMP stimulated nucleotide phosphodiesterase;

KW bovine brain; hormones; neurotransmitters; transmission regulation;

KW antibodies; enzyme purification; clone p12-3a.

XX Bos taurus.

XX US5389527-A.

PN 14-FEB-1995.

XX 20-APR-1992; 92US-0872644.

PR 19-APR-1991; 91US-0688356.

PR 20-APR-1992; 92US-0872644.

XX (UNIW ) UNIV WASHINGTON.

Beavo JA, Charbonneau H, Sonnenburg WK;

WPI; 1995-090205/12.

DR N-PSDB; AAQ83969.

XX New nucleic acid encoding cyclic-GMP stimulated nucleotide

PT phosphodiesterase - and related vectors and transformed cells,

PT useful for screening cpds. for phosphodiesterase modulating

PT activity

XX Example 3; Columns 55-60; 69pp; English.

PS AAQ83969 encodes AAR69720 the bovine brain cyclic-GMP stimulated

CC nucleotide phosphodiesterase (Cam PDE) clone p12.3a. Eukaryotic cells

CC that express Cam PDE can be used to screen cpds. for the ability to

CC modulate Cam PDE activity. Cam PDEs are involved in regulating

CC the transmission of information from hormones, neurotransmitters

CC or other systems that use cyclic nucleotides as messengers.

CC Antibodies raised against Cam PDE can be used for enzyme purificn.,

QY 19 LRYMVKQLENGEINIEELKKNLEYTASLEAVYIDETROILDELOELRSDAVPSEVR 78  
DB 38 LRYMVKQLENGEINIEELKKNLEYTASLEAVYIDETROILDELOELRSDAVPSEVR 97  
QY 79 DWLASTFTQOARAKARRAEKPKRSIVHAVAQAGIFVERMFRRTYTSVGPPTYSTAVLNCL 138  
DB 98 DWLASTFTQOARAKARRAEKPKRSIVHAVAQAGIFVERMFRRTYTSVGPPTYSTAVLNCL 156  
QY 139 KNLDLWCFDVFSLNQAADHALRTIVFELLTRHNLISREKIPVFLMFLSDALETGYGY 198  
DB 157 KNLDLWCFDVFSLNQAADHALRTIVFELLTRHNLISREKIPVFLMFLSDALETGYGY 216  
QY 199 KNPYHNQIHAADVDTQVHCFLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSPHIQ 258  
DB 217 KNPYHNQIHAADVDTQVHCFLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSPHIQ 276  
QY 259 KSECAIVYNDRSVLENNHHSVFRMLQDDMMNIFNLTKDEFVELRALVIEWVLATDMSC 318  
DB 277 KSECAIVYNDRSVLENNHHSVFRMLQDDMMNIFNLTKDEFVELRALVIEWVLATDMSC 336  
QY 319 HFQOVKMTALQQLERIDKPKALLSLLHAADISHTPKQWLHVRWTKALMEEFPRQGD 378  
DB 337 HFQOVKMTALQQLERIDKPKALLSLLHAADISHTPKQWLHVRWTKALMEEFPRQGD 396  
QY 379 EAEGLPFPPLCDRTSTLVAQSIQIGFIDIVEPTFSLTDVAEKSVQPLADESKSNOP 438  
DB 397 EAEGLPFPPLCDRTSTLVAQSIQIGFIDIVEPTFSLTDVAEKSVQPLADESKSNOP 456  
QY 439 SFQWQPSLDVEGPNPDVFSRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 498  
DB 457 SFQWQPSLDVEGPNPDVFSRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 516  
QY 499 EAPPSPAEDEHNGNGLD 516  
DB 517 EAPPSPAEDEHNGNGLD 534

RESULT 4

AAW18038

ID AAW18038 standard; protein; 534 AA.

XX AC AAW18038;

XX 25-MAR-2003 (updated)

DT 31-JUL-1997 (first entry)

XX Bovine brain 63 kDa Ca2+/calmodulin stimulated phosphodiesterase.

DE Ca2+/calmodulin stimulated cyclic nucleotide phosphodiesterase enzyme;

KW calcium ion; Cam-PDE; antibody; cow.

XX Bos taurus.

XX US5602019-A

PN 11-FEB-1997.

XX 29-AUG-1994; 94US-0297510.

XX 20-APR-1992; 92US-0872644.

PR 19-APR-1991; 91US-0688356.

PR 29-AUG-1994; 94US-0297510.

XX (UNIW ) UNIV WASHINGTON.

XX Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;

XX WPI; 1997-131799/12.

XX N-PSDB; AAT67200.

XX DNA encoding bovine and human phosphodiesterase enzymes - stimulated

PT by calcium/calmodulin, useful for recombinant prodn. of the enzymes

Query Match 92.88; Score 2484.5; DB 16; Length 534;

Best Local Similarity 96.0%; Pred. No. 1.2e-226;

Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;



Db 397 EAEGLPFLCDRTSTLVAQSIGFIDFIVEPTFSLTDAEKSQVPTGDDDSKSNQP 456  
QY 439 SFQWRQPSLDVEGDPNPDVVSFRSTWVKRIQENKQKWKERAASGITNOMSIDELSPCEE 498  
Db 457 SFQWRQPSLDVEGDPNPDVVSFRSTWVKRIQENKQKWKERAASGITNOMSIDELSPCEE 516  
QY 499 EAPSPAEDHNQNGNLD 516  
Db 517 EAPSPAEDHNQNGNLD 534

RESULT 6  
AAW77039  
ID AAW77039 standard; Protein; 534 AA.  
XX  
AC AAW77039;  
XX  
DT 09-NOV-1998 (first entry)  
XX  
DE Bovine brain Ca2+/calmodulin stimulated phosphodiesterase clone p12.  
KW Cow Ca2+ stimulated phosphodiesterase;  
KW Calmodulin stimulated phosphodiesterase; therapeutic; antibody.  
XX  
OS Bos sp.  
XX  
PN US5789553-A.  
PD 04-AUG-1998.  
XX  
XX 31-MAY-1995. 950S-0455526.  
XX 28-APR-1992; 920S-0872644.  
PR 19-APR-1991; 910S-0688356.  
PR 29-AUG-1994; 940S-0297494.  
PR 31-MAY-1995; 950S-0455526.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;  
XX  
XX WPI: 1998-446185/38.  
DR N-PSDB; AAV48196.  
XX  
PT Antibody to phosphodiesterase polypeptide - useful for purification  
PT or detection of polypeptide  
XX  
XX Example 3; Column 53-58; 68pp; English.  
XX  
CC The bovine brain Ca2+/calmodulin stimulated phosphodiesterase protein  
CC shows sequence alignment to the 63 kDa protein. The phosphodiesterase is  
CC one of several phosphodiesterases isolated in this invention, used to  
CC transform host cells, preferably mammalian or yeast cells. The  
CC recombinant proteins and fragments produced can be used for therapeutic,  
CC diagnostic, and prognostic purposes and will provide the basis for  
CC preparation of monoclonal and polyclonal antibodies. An antibody  
CC specific for the Ca2+/calmodulin-stimulated cyclic nucleotide  
CC phosphodiesterase (PDE) polypeptide is useful for affinity purification  
CC or detection of the polypeptide and is selective only for the  
CC Ca2+/calmodulin stimulated cyclic nucleotide PDE polypeptide.  
XX  
SQ Sequence 534 AA;  
Query Match 92.8%; Score 2484.5; DB 19; Length 534;  
Best Local Similarity 96.0%; Pred. No. 1.2e-226;  
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;  
QY 19 LRYMWKQLENGEINTEELKKNLEYTASLLEAVYIDETQILDTDELOELRSDAVPSEVR 78  
Db 38 LRYMWKQLENGEINTEELKKNLEYTASLLEAVYIDETQILDTDELOELRSDAVPSEVR 97  
QY 79 DMLASTFTQQRAGKRAEKKPKFSIVHVAQGIFFVERMFRRTVTSVGPITYSTAVLNCL 138  
||||||| ||||| :|||||||

Db 98 DMLASTFTQQRAGK -PSEKPKFSIVHVAQGIFFVERMFRRTVTSVGPITYSTAVLNCL 156  
QY 139 KNLDWCDFVSLNQAADHALRTIVFELLTRHNLISRPKIPTVFLMSFLDALETGYGKY 198  
Db 157 KNVDWCDFVSLNQAADHALRTIVFELLTRHNLISRPKIPTVFLMSFLDALETGYGKY 216  
QY 199 KNPYHNOIHAADVTQVHCFLLRGTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSPHIQT 258  
Db 217 KNPYHNOIHAADVTQVHCFLLRGTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSPHIQT 276  
QY 259 KSECAIVYNDRSVLEHHHISVFRMLQDDMMIFNLTKDEFVELRALVIEVMTATDMSC 318  
Db 277 KSECAILYNDRSVLEHHHISVFRMLQDDMMIFNLTKDEFVELRALVIEVMTATDMSC 336  
QY 319 HFQOVKTMKTALQQLERIDKPKALSLLHAADSHPTKQWLVSHTWTKALMEEFPRQGD 378  
Db 337 HFQOVKTMKTALQQLERIDKPKALSLLHAADSHPTKQWLVSHTWTKALMEEFPRQGD 396  
QY 379 EAEGLPFLCDRTSTLVAQSIGFIDFIVEPTFSLTDAEKSQVPLADEDSKSNQP 438  
Db 397 EAEGLPFLCDRTSTLVAQSIGFIDFIVEPTFSLTDAEKSQVPTGDDDSKSNQP 456  
QY 439 SFQWRQPSLDVEGDPNPDVVSFRSTWVKRIQENKQKWKERAASGITNOMSIDELSPCEE 498  
Db 457 SFQWRQPSLDVEGDPNPDVVSFRSTWVKRIQENKQKWKERAASGITNOMSIDELSPCEE 516  
QY 499 EAPSPAEDHNQNGNLD 516  
Db 517 EAPSPAEDHNQNGNLD 534

RESULT 7  
AAW71223  
ID AAW71223 standard; Protein; 534 AA.  
XX  
AC AAW71223;  
XX  
DT 29-OCT-1998 (first entry)  
XX  
DE 63 kDa CaM-PDE encoded by clone p12.3a.  
XX  
KW Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; CaM-PDE;  
KW assay; identification; modification; enzymatic activity; modulator.  
XX  
OS Bos sp.  
XX  
PN US5800987-A.  
XX  
PD 01-SEP-1998.  
XX  
XX 31-MAY-1995; 950S-0455525.  
XX  
XX 20-APR-1992; 920S-0872644.  
XX 19-APR-1991; 910S-0688356.  
XX 29-AUG-1994; 940S-0297494.  
XX 31-MAY-1995; 950S-0455525.  
XX (UNIW ) UNIV WASHINGTON.  
XX  
XX Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;  
PI WPI: 1998-494762/42.  
DR N-PSDB; AAV54753.  
XX  
XX Identification of modulators of Calcium/calmodulin sensitive cyclic  
PT nucleotide phosphodiesterase - uses recombinant cells expressing the  
PT enzyme and monitoring protein expression in the presence of  
XX potential modulators  
PS Example 3; Columns 59-62; 69pp; English.  
XX  
CC The present sequence represents a 63 kDa Ca2+/calmodulin sensitive cyclic  
CC nucleotide phosphodiesterase (CaM-PDE) from bovine brain. CaM-PDE enzymes

CC catalyse the hydrolysis of cyclic nucleotides and as such control their  
 CC intracellular level, they are controlled by second messengers e.g. Ca<sup>2+</sup>  
 CC and calmodulin and transmembrane signals and through pathways involving  
 CC these, regulate flow of information from extracellular hormones,  
 CC neurotransmitters and other signals using cyclic nucleotides as  
 CC messengers. The specification describes an assay for identifying a  
 CC chemical agent which modifies the enzymatic activity of a mammalian  
 CC Cam-PDE. The assays are useful for identifying modulators of Cam-PDEs.  
 CC The assay is carried out by incubating cells expressing Cam-PDE with the  
 CC suspected modulator and measuring its effect e.g. monitoring the  
 CC hydrolysis of cAMP and/or cGMP.

XX Sequence 534 AA;

Query Match 92.8%; Score 2484.5; DB 19; Length 534;  
 Best Local Similarity 96.0%; Pred. No. 1.2e-226;  
 Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 19 LRYMKQLENGEINIEELKKNLEYTASLLEAVYIDETROIQLDTEDELOELRSDAVPSEVR 78  
 DB 38 LRYMKQLENGEINIEELKKNLEYTASLLEAVYIDETROIQLDTEDELOELRSDAVPSEVR 97  
 QY 79 DWLASTFTQOARAKRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPSTYAVLNCL 138  
 DB 98 DWLASTFTQOARAKRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPSTYAVLNCL 156  
 QY 139 KNLDLWCFDVSFSLNOADDHALRTIVFELLTRNHLISRPKIPVFLMSFLDALETGYGKY 198  
 DB 157 KNVDLWCFDVSFSLNOADDHALRTIVFELLTRNHLISRPKIPVFLMSFLDALETGYGKY 216  
 QY 199 KNPYHNOIHAADYTOTVHCFLRTGCVHCLSEIELLAIIFAAAIHDYHGTGTTNSPHIQT 258  
 DB 217 KNPYHNOIHAADYTOTVHCFLRTGCVHCLSEIELLAIIFAAAIHDYHGTGTTNSPHIQT 276  
 QY 259 KSECAIYVNDRSVLENHHISSVFRMMDMMNIFNLTKDEFVELRALVIEMVLATDMSC 318  
 DB 277 KSECAIYVNDRSVLENHHISSVFRMMDMMNIFNLTKDEFVELRALVIEMVLATDMSC 336  
 QY 319 HFQOVTKMTALQOERIDPKALSLLLHAADISHPTKQWLHRSWTKALMEEFFRQGDK 378  
 DB 337 HFQOVTKMTALQOERIDPKALSLLLHAADISHPTKQWLHRSWTKALMEEFFRQGDK 396  
 QY 379 EAEGLGPFSPICDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKKNOP 438  
 DB 397 EAEGLGPFSPICDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKKNOP 456  
 QY 439 SFQWRQPSLDVEGDPNDPVVSPRSTWTKYIQENKQKWKERAAAGITNOMSIDELSPCEE 498  
 DB 457 SFQWRQPSLDVEGDPNDPVVSPRSTWTKYIQENKQKWKERAAAGITNOMSIDELSPCEE 516  
 QY 499 EAPPSPAEDHNGNLD 516  
 DB 517 EAPPSPAEDHNGNLD 534

RESULT 8

ID AAW60751 standard; Protein; 534 AA.

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XX US5776752-A.  
 PN  
 XX  
 PD 07-JUL-1998.  
 XX  
 PF 07-JUN-1995; 95US-0479532.  
 XX  
 PR 20-APR-1992; 92US-0872644.  
 XX  
 PR 19-APR-1991; 91US-0688356.  
 XX  
 PR 29-AUG-1994; 94US-0297494.  
 XX  
 XX (UNIW ) UNIV WASHINGTON.

PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;  
 XX  
 XX WPI; 1998-398038/34.  
 DR  
 DR N-PSDB; #AV36148.  
 XX

PT New calmodulin and calcium stimulated cyclic nucleotide  
 PT phosphodiesterase - used e.g to identify selective modulators,  
 PT potentially useful as e.g. cardiotonic, antidepressant,  
 PT antihypertensive agents  
 XX

PS Claim 3: Columns 57-60; 69pp; English.

XX The present sequence represents 63 kDa calcium ion/calmodulin stimulated  
 CC cyclic nucleotide phosphodiesterase (Cam-PDE) polypeptide, isolated from  
 CC bovine brain. Cam-PDEs are characterised by their responsiveness  
 CC to intracellular calcium, which leads to a decreased intracellular  
 CC concentration of cAMP and/or cGMP. Cam-PDEs, and their fragments or  
 CC synthetic peptides, are used in therapy, prognosis and diagnosis. They  
 CC are also used to generate specific antibodies useful as immunoassay  
 CC reagents for detecting the protein or for affinity purification and for  
 CC implicating specific modulators of Cam-PDE activity. Cam-PDEs are  
 CC implicated in signalling involving extracellular hormones and  
 CC neurotransmitters, so selective inhibitors are potentially useful as  
 CC cardiotonic, antidepressant, antihypertensive and antithrombotic agents.

XX Sequence 534 AA;

Query Match 92.8%; Score 2484.5; DB 19; Length 534;  
 Best Local Similarity 96.0%; Pred. No. 1.2e-226;  
 Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 19 LRYMKQLENGEINIEELKKNLEYTASLLEAVYIDETROIQLDTEDELOELRSDAVPSEVR 78  
 DB 38 LRYMKQLENGEINIEELKKNLEYTASLLEAVYIDETROIQLDTEDELOELRSDAVPSEVR 97  
 QY 79 DWLASTFTQOARAKRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPSTYAVLNCL 138  
 DB 98 DWLASTFTQOARAKRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPSTYAVLNCL 156  
 QY 139 KNLDLWCFDVSFSLNOADDHALRTIVFELLTRNHLISRPKIPVFLMSFLDALETGYGKY 198  
 DB 157 KNVDLWCFDVSFSLNOADDHALRTIVFELLTRNHLISRPKIPVFLMSFLDALETGYGKY 216  
 QY 199 KNPYHNOIHAADYTOTVHCFLRTGCVHCLSEIELLAIIFAAAIHDYHGTGTTNSPHIQT 258  
 DB 217 KNPYHNOIHAADYTOTVHCFLRTGCVHCLSEIELLAIIFAAAIHDYHGTGTTNSPHIQT 276  
 QY 259 KSECAIYVNDRSVLENHHISSVFRMMDMMNIFNLTKDEFVELRALVIEMVLATDMSC 318  
 DB 277 KSECAIYVNDRSVLENHHISSVFRMMDMMNIFNLTKDEFVELRALVIEMVLATDMSC 336  
 QY 319 HFQOVTKMTALQOERIDPKALSLLLHAADISHPTKQWLHRSWTKALMEEFFRQGDK 378  
 DB 337 HFQOVTKMTALQOERIDPKALSLLLHAADISHPTKQWLHRSWTKALMEEFFRQGDK 396  
 QY 379 EAEGLGPFSPICDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKKNOP 438  
 DB 397 EAEGLGPFSPICDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKKNOP 456  
 QY 439 SFQWRQPSLDVEGDPNDPVVSPRSTWTKYIQENKQKWKERAAAGITNOMSIDELSPCEE 498

Db 457 SFQWRQPSLDVEGDPNPDVVSFRSTWTKYIOENKQKWKRAASGITNOMSIDELSPCEE 516  
 QY 499 EAPSPAEDENHONGNLD 516  
 Db 517 EAPSPAEDENHONGNLD 534

## RESULT 9

AAAY80977  
 ID AAY80977 standard; Protein: 534 AA.

XX AC AAY80977;

XX DT 05-JUN-2000 (first entry)

XX DE Bovine brain 63 kD CaM-PDE clone p12.3a protein, SEQ ID NO:27.

XX KW Phosphodiesterase; calcium; calmodulin; cyclic guanine monophosphate;  
 KW cGMP; cyclic nucleotide; messenger; signal transduction; regulation;  
 KW inhibitor; cardiotonic; antidepressant; antihypertensive;  
 KW antithrombotic.

XX OS Bos taurus.

XX PN US6015677-A.

XX PD 18-JAN-2000.

XX PF 25-AUG-1998; 98US-0139491.

XX PR 20-APR-1992; 92US-0872644.

XX PR 29-AUG-1994; 94US-0297494.

XX PR 31-MAY-1995; 95US-0455525.

XX PR 19-APR-1991; 91US-0688356.

XX PA (UNIW ) UNIV WASHINGTON.

XX PI Charbonneau H, Sonnenburg WK, Bentley KJ, Beavo JA;

XX DR WPI: 2000-181142/16.

XX DR N-PSDB; AAZ90372.

XX PT Assay for inhibitors of cyclic guanine monophosphate-stimulated

XX PT nucleotide phosphodiesterase, potentially useful as cardiotonic agents,

XX PT from their ability to alter a heat-shock phenotype

XX PS Example III; Column 57-60; 69pp; English.

XX CC The invention relates to purified and isolated nucleotide sequences  
 CC encoding mammalian Ca2+/calmodulin-stimulated phosphodiesterases  
 CC (CaM-PDEs) and cyclic guanine monophosphate (cGMP)-stimulated  
 CC phosphodiesterases (cGS-PDEs). In particular the invention relates to an  
 CC assay for identifying chemicals that modify the enzymatic activity of  
 CC a mammalian cGS-PDE. The PDEs catalyse the hydrolysis of cyclic  
 CC nucleotides to their corresponding 5'-nucleoside monophosphates. In this  
 CC way they control the cellular concentration of cyclic nucleotides,  
 CC thereby regulating the flow of information from extracellular hormones,  
 CC neurotransmitters or other signals that use cyclic nucleotides as  
 CC messengers. The PDEs in turn are regulated by transmembrane signals  
 CC or second messenger ligands such as Ca2+ or cGMP. Inhibitors of these  
 CC enzymes are potentially useful as cardiotonics, antidepressants,  
 CC antihypertensives or antithrombotics. The method of the invention can  
 CC identify specific inhibitors of particular isoforms of cGS-PDEs.  
 CC Sequences AAY80968, AAY80972, AAY80975, AAY80984-Y80986, and  
 CC AAY80988-Y80990 represent isoforms of CaM-PDEs and cGS-PDEs from bovines  
 CC and humans.

XX SQ Sequence 534 AA;

Query Match 92.8%; Score 2484.5; DB 21; Length 534;

Best Local Similarity 96.0%; Pred. No. 1.2e-226;

Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 19 LRYMVKQLENGEINIEELKKNLEYTASLEAVYIDETROIILDTDEQLRSDAVPSEVR 78  
 Db 38 LRYMVKQLENGEINIEELKKNLEYTASLEAVYIDETROIILDTDEQLRSDAVPSEVR 97  
 QY 79 DWLASTFTQARAKGRRAEKPFRSIVHVAQAGIFVERMPFRRTVTSVGPTYSTAVLNCL 138  
 Db 98 DWLASTFTQOTRAGK-PSEKPKFRSIVHVAQAGIFVERMPFRRTVTSVGPTYSTAVLNCL 156  
 QY 139 KNLDLWCFDVSLSNOAADDHALRTIVFELLTRHNLSIRFKIPTVFLMSFLDALETGYGYK 198  
 Db 157 KNVDLWCFDVSLSNRAADDHALRTIVFELLTRHNLSIRFKIPTVFLMTFLDALETGYGYK 216  
 QY 199 KNPYHNOIHAADVOTVHCFLIRTCGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHQT 258  
 Db 217 KNPYHNOIHAADVOTVHCFLIRTCGMVHCLSEIEVLAIIFAAAIHDYEHGTGTTNSFHQT 276  
 QY 259 KSECAIVYNDRSVLNHHISSVFRMLQDDNMNIFNLTKDEFVELRALVIEMLATDMSC 318  
 Db 277 KSECAILYNDRSVLNHHISSVFRMQDDNMNIFNLTKDEFVELRALVIEMLATDMSC 336  
 QY 319 HFQVKYTKMTALQQLERIDKPKALSLLHAADISHPTKQWLVHSRWTALMEEFFRQGDK 378  
 Db 337 HFQVKYSMTALQQLERIDKSKALSLLHAADISHPTKQWSVHSRWTALMEEFFRQGDK 396  
 QY 379 EAEGLPSPICDRSTSLVAOSIQGIDFIVEPTESVLTVAEKSQVQLADEDSKSNQP 438  
 Db 397 EAEGLPSPICDRSTSLVAOSIQGIDFIVEPTESVLTVAEKSQVQTGDDDSKSNQP 456  
 QY 439 SFQWRQPSLDVEGDPNPDVVSFRSTWTKYIOENKQKWKRAASGITNOMSIDELSPCEE 498  
 Db 457 SFQWRQPSLDVEGDPNPDVVSFRSTWTKYIOENKQKWKRAASGITNOMSIDELSPCEE 516  
 QY 499 EAPSPAEDENHONGNLD 516  
 Db 517 EAPSPAEDENHONGNLD 534

## RESULT 10

ABU58716  
 ID ABU58716 standard; Protein: 534 AA.

XX AC ABU58716;

XX DT 15-APR-2003 (first entry)

XX DE Bovine brain 63kDa CaM-PDE variant #1.

XX KW Cow; Ca2+/calmodulin stimulated phosphodiesterase; enzyme;  
 KW Cam-PDE; 59KDa CaM-PDE; 61kDa CaM-PDE; 63kDa CaM-PDE; cGS-PDE;  
 KW cyclic-GMP-stimulated phosphodiesterase; cardiotonic agent;  
 KW antidepressant; anti-hypertensive; anti-thrombotic.

XX OS Bos taurus.

XX PN US2002151024-A1.

XX PD 17-OCT-2002.

XX PF 18-JUN-2001; 2001US-0883825.

XX PR 20-APR-1992; 92US-0872644.

XX PR 31-MAY-1995; 95US-0455526.

XX PR 28-JUL-1998; 98US-0123783.

XX PR 19-APR-1991; 91US-0688356.

XX PA (UNIW ) UNIV WASHINGTON.

XX PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;

XX DR WPI; 2003-198291/19.

XX DR N-PSDB; ABX78849.

PT New purified and isolated DNA sequence encoding a mammalian  
 PT calcium/calmodulin- or cyclic GMP-stimulated cyclic nucleotide  
 PT phosphodiesterase polypeptide, useful for therapeutic, diagnostic and  
 PT prognostic applications -  
 XX  
 XX  
 XX Example 3; Page 32-33; 71pp; English.

XX The invention relates to purified and isolated polynucleotide sequence  
 CC encoding a mammalian Ca<sup>2+</sup>/calmodulin- or cyclic GMP-stimulated cyclic  
 CC nucleotide phosphodiesterase polypeptide (CaMP-PDE and CGS-PDE).  
 CC Also included are a DNA vector comprising the novel DNA sequence, a host  
 CC cell transformed with the polynucleotide sequence, a polypeptide product  
 CC of the expression in the transformed host cell, an antibody specifically  
 CC immunoreactive with the polypeptide and assay methods for identifying a  
 CC chemical agent which modifies the enzymatic activity of a mammalian  
 CC CaMP-PDE or CGS-PDE. Disclosed are the cDNA and protein sequences  
 CC of bovine 59kDa CaM-PDE, 61kDa CaM-PDE, 63kDa CaM-PDE, CGS-PDE and  
 CC human 61kDa CaM-PDE and CGS-PDE. The DNA sequence is useful for producing  
 CC a polypeptide having the enzymatic activity of a mammalian CaM-PDE or  
 CC CGS-PDE which is used in the preparation of antibodies and prognostic  
 CC applications and in the preparation of antibodies. Isolated chemical  
 CC agents which are inhibitors of PDEs may have anti-depressant, anti-  
 CC hypertensive or anti-thrombotic activities or may be cardiotoxic agents.  
 CC The present sequence is a Bovine CaM-PDE or CGS-PDE (or fragment) of the  
 CC invention.

XX Sequence 534 AA;

Query Match 92.6%; Score 2484.5; DB 24; Length 534;  
 Best Local Similarity 96.6%; Pred. No. 1.2e-226;  
 Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;  
 QY 19 LRYWVKQLENGEINTEELKKNLEYTASLEAVYIDETROILOLDELQELSDAVPSEVR 78  
 DB 38 LRYWVKQLENGEINTEELKKNLEYTASLEAVYIDETROILOLDELQELSDAVPSEVR 97  
 QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGYTSTAVLNCL 138  
 DB 98 DWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGYTSTAVLNCL 156  
 QY 139 KNLDLWCFDVFSLNQADDAHALRTIVFELLTRHNLISRFKIPVFLMSFLDALETGYGKY 198  
 DB 157 KNVDLWCFDVFSLNQADDAHALRTIVFELLTRHNLISRFKIPVFLMSFLDALETGYGKY 216  
 QY 199 KNPYHNQIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHIQT 258  
 DB 217 KNPYHNQIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHIQT 276  
 QY 259 KSCAIVYNDRSVLENHHISSVFRMQDDENIFNLTKDFVELRALVEMVLATDMSC 318  
 DB 277 KSCAIVYNDRSVLENHHISSVFRMQDDENIFNLTKDFVELRALVEMVLATDMSC 336  
 QY 319 HFQOVKMTALQQLERIDKPKALSLLLHAADISHPTKOWLVHSRWTKALMEEFFRQGDK 378  
 DB 337 HFQOVKMTALQQLERIDKPKALSLLLHAADISHPTKOWLVHSRWTKALMEEFFRQGDK 396  
 QY 379 EAELGLPFPCLDRTSTLVAQSQIGFIDFIVEPTFVLTVDVAEKSVQPLADEDSKKNOP 438  
 DB 397 EAELGLPFPCLDRTSTLVAQSQIGFIDFIVEPTFVLTVDVAEKSVQPLADEDSKKNOP 456  
 QY 439 SFQWRQPSLDVEGDPNDVFSRSTWVKRIQENKQWKRAASGITNOMSDIDELSPCEE 498  
 DB 457 SFQWRQPSLDVEGDPNDVFSRSTWVKRIQENKQWKRAASGITNOMSDIDELSPCEE 516  
 QY 499 EAPPSPAEDHNGNGLD 516  
 DB 517 EAPPSPAEDHNGNGLD 534

RESULT 11

AAR28404  
 ID AAR28404 standard; Protein; 534 AA.  
 XX

AC AAR28404;  
 XX 25-MAR-2003 (updated)  
 DT 19-MAR-1993 (first entry)  
 XX  
 XX 63 kD CaM PDE from clone p12.3a from bovine brain.  
 XX  
 XX Calcium/calmodulin; stimulated; cyclic; nucleotide;  
 KW phosphodiesterase.  
 KW Bos taurus.  
 OS  
 XX Key Location/Qualifiers  
 FT Region 44..57  
 FT /note= "homology with aligned peptides from 63kD CaM PDE"  
 FT Region 277..292  
 FT /note= "homology with aligned peptides from 63kD CaM PDE"  
 XX  
 XX WO9218541-A1.  
 XX  
 XX 29-OCT-1992.  
 XX  
 XX 20-APR-1992; 92WO-US03222.  
 XX  
 XX 19-APR-1991; 91US-0688356.  
 XX  
 XX (UNIW ) UNIV WASHINGTON.  
 PA  
 XX Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;  
 PI WPI; 1992-382051/46.  
 XX N-PSDB; AAQ30175.  
 DR  
 XX New DNA encoding mammalian cyclic nucleotide phospho-di:esterase  
 PT - and derived vectors and host cells, useful for screening cpds.  
 PT for inhibitory or activating activity  
 XX  
 XX Example 3; Page 76; 133pp; English.  
 XX  
 XX Oligonucleotide 63-1s, a fully redundant 23-mer was used to screen a  
 CC total bovine brain cDNA library in lambda ZAP II. A total of 21  
 CC putative positives were picked and rescreened with the probe from  
 CC plasmid p11.5b. One positive was obtd. designated p12.3a, which  
 CC codes for a protein sequence with most of the aligned peptides  
 CC isolated from bovine 63 kD CaM PDE.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 534 AA;  
 Query Match 92.6%; Score 2478.5; DB 13; Length 534;  
 Best Local Similarity 95.6%; Pred. No. 4.3e-226;  
 Matches 476; Conservative 12; Mismatches 9; Indels 1; Gaps 1;  
 QY 19 LRYWVKQLENGEINTEELKKNLEYTASLEAVYIDETROILOLDELQELSDAVPSEVR 78  
 DB 38 LRYWVKQLENGEINTEELKKNLEYTASLEAVYIDETROILOLDELQELSDAVPSEVR 97  
 QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGYTSTAVLNCL 138  
 DB 98 DWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGYTSTAVLNCL 156  
 QY 139 KNLDLWCFDVFSLNQADDAHALRTIVFELLTRHNLISRFKIPVFLMSFLDALETGYGKY 198  
 DB 157 KNVDLWCFDVFSLNQADDAHALRTIVFELLTRHNLISRFKIPVFLMSFLDALETGYGKY 216  
 QY 199 KNPYHNQIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHIQT 258  
 DB 217 KNPYHNQIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHIQT 276  
 QY 255 KSCAIVYNDRSVLENHHISSVFRMQDDENIFNLTKDFVELRALVEMVLATDMSC 318  
 DB 277 KSCAIVYNDRSVLENHHISSVFRMQDDENIFNLTKDFVELRALVEMVLATDMSC 336



QY 319 HFQVQVTKMTALQQLERIDKPKALSLLHAADISHPTKQWLHVSRWTKALMEEFPRQGD 378  
 Db 337 HFQVQVSMKMTALQQLERIDKPKALSLLHAADISHPTKQWVSRWTKALMQEPRQGD 396  
 QY 379 EAEGLPSPCLDRSTSLVAQSQIGFIDFIVEPTFSLTDLVAEKSVQPLADEDSKKNOP 438  
 Db 397 EAEGLPSPCLDRSTSLVAQSQIGFIDFIVEPTFSLTDLVAEKSVQPTGDDDSKKNOP 456  
 QY 439 SFQWRQPSLDVEGPNPDVVSFRSTWTKRIQENKQKRAASGITNOMSIDELSPCEE 498  
 Db 457 SFQWRQPSLDVEGPNPDVVSFRSTWTKRIQENKQKRAASGITNOMSIDELSPCEE 516  
 QY 499 EAPSPAPAEHNNQNL 516  
 Db 517 EAPSPAPAEHNNQNL 534

## RESULT 12

.ID AAR69715 standard; Protein; 514 AA.

XX AAR69715;

DT 25-MAR-2003 (updated)

DT 11-OCT-1995 (first entry)

DE Cyclic-GMP stimulated nucleotide PDE clone p59KCAMPDE-2.

KW Cyclic-GMP stimulated nucleotide phospho-diesterase;  
 KW bovine lung; hormones; neurotransmitters; transmission regulation;  
 KW antibodies; enzyme purification; clone p59CAMPDE-2.

XX Bos taurus.

XX US5389527-A.

XX 14-FEB-1995.

XX 20-APR-1992; 92US-0872644.

XX 19-APR-1991; 91US-0688356.

XX 20-APR-1992; 92US-0872644.

XX (UNIW ) UNIV WASHINGTON.

XX Beavo JA, Charbonneau H, Sonnenburg WK;

XX WPI; 1995-090205/12.

DR N-PSDB; AAQ83964.

XX New nucleic acid encoding cyclic-GMP stimulated nucleotide  
 PT phospho-diesterase - and related vectors and transformed cells,  
 PT useful for screening cpds. for phospho-di:esterase modulating  
 PT activity

XX Example 2; Columns 43-48; 69pp; English.

XX AAQ83964 encodes AAR69715 bovine lung cyclic-GMP stimulated nucleotide  
 CC phospho-diesterase (Cam PDE) clone p59KCAMPDE-2. Eukaryotic cells  
 CC that express Cam PDE can be used to screen cpds. for the ability to  
 CC modulate Cam PDE activity. Cam PDEs are involved in regulating  
 CC the transmission of information from hormones, neurotransmitters  
 CC or other systems that use cyclic nucleotides as messengers.  
 CC Antibodies raised against Cam PDE can be used for enzyme purific.,  
 CC or determination.

CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 514 AA;

## Query Match

Best Local Similarity 61.2%; Score 1636.5; DB 16; Length 514;

Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

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 Db 1 MDDHVTIRKHLORPIERLRLCLVKLEKGDVNVIDLKNIEYAAVLEAVYIDETRLILD 60  
 QY 61 TEDELOELRSADVSEVRDLASTTQQRARAKRAEERKPRRSIVHAVQAGIFVERMFR 120  
 Db 61 TDDELSDIQSDSPVSEVRDLASTTFRKMGMMKKSEKPRRSIVHVQAGIFVERMYR 120  
 QY 121 RYTSVSGPTYSTAVLNCNLKNDLWCFVFSLNAAADHALRTIVFELTRHNLISRFKIP 180  
 Db 121 KSYHVMGLAYPAVIVITLKDVKNSFDVFNALNEASGEHSLKPMIYELTRYDLINRFKIP 180  
 QY 181 TVFLMSFLDALETGYGKYKNPYHNIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAA 240  
 Db 181 VSLCIAFAEALEVGYSKYKNPYHNIHAADVTQTVHYIMLHTGIMHMLTELEILAMVFAA 240  
 QY 241 AIHDEHTGTNSFIQTKSECAIVYNDRSVLENHIISSVFLMQDDENINILTKDEF 300  
 Db 241 AIHDEHTGTNNFIQTRSDVAILYNDRSVLENHVSAAAYRLMQDEENNVILNSKDDW 300  
 QY 301 VELRALVTEMVLATDMSCHFOQVTKMTALQQLERIDKPKALSLLHAADISHPTKQWL 360  
 Db 301 RDLRLNVTEMVLSTDMSGHFOQIKNIRNSLQOPEGLDKAKTMSLILHAADISHPAKSWL 360  
 QY 361 HSRWTKALMEEFPRQDKEAEELGLPSPCLDRSTSLVAQSQIGFIDFIVEPTFSLTDT 420  
 Db 361 HHRWTMALMEEFPRQDKEAEELGLPSPCLDRKSTWVAQSQIGFIDFIVEPTFSLTDT 420  
 QY 421 EKSVOPLADEDSKKNQPSFQWRQPSLDVEGCD-----PNPDVVSFRSTWVKRIQE 471  
 Db 421 EKIIPLIEEDSKTKTPSYGASRRGNMKGTNDGTYSPTYSLASVDLAKSFKNLSLDIIQ 480  
 QY 472 NKQWKERAASGITNOMSIDELSPCEE 499  
 Db 481 NKRWKEAAQGEPPDHKNSDLVNAEEK 508

## RESULT 13

AAW18037

ID AAW18037 standard; protein; 514 AA.

XX AAW18037;

XX 25-MAR-2003 (updated)

DT 31-JUL-1997 (first entry)

DE Bovine lung 59 kDa Ca2+/calmodulin stimulated phosphodiesterase.

KW Ca2+/calmodulin stimulated cyclic nucleotide phosphodiesterase enzyme;  
 KW calcium ion; Cam-PDE; antibody; cow.

XX Bos taurus.

XX US5602019-A.

XX 11-FEB-1997.

XX 29-AUG-1994; 94US-0297510.

XX 20-APR-1992; 92US-0872644.

PR 19-APR-1991; 91US-0688356.

XX 29-AUG-1994; 94US-0297510.

XX (UNIW ) UNIV WASHINGTON.

XX Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;

XX WPI; 1997-131799/12.

DR N-PSDB; AAT67199.

XX DNA encoding bovine and human phosphodiesterase enzymes - stimulated  
 PT by calcium/calmodulin, useful for recombinant prodn. of the enzymes





**THIS PAGE BLANK (0010),**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2003, 01:06:37 ; Search time 43 Seconds  
(without alignments)  
507.730 Million cell updates/sec

Title: US-09-663-481-1  
Perfect score: 2676  
Sequence: 1 MANPVPVQRSHLQGFILRL.....BEEAPPSAEDEHNQNLID 516

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2.6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2.6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2.6/ptodata/1/1aa/PCTUS\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2592	96.5	536	2	US-08-940-332-2
2	2484.5	92.8	534	1	US-07-872-644-27
3	2484.5	92.8	534	1	US-08-297-494-27
4	2484.5	92.8	534	1	US-08-297-510-27
5	2484.5	92.8	534	1	US-08-479-532-27
6	2484.5	92.8	534	1	US-08-455-526-27
7	2484.5	92.8	534	1	US-08-455-525-27
8	2484.5	92.8	534	3	US-09-139-491-27
9	2484.5	92.8	534	5	PCT-US92-03222-27
10	1636.5	61.2	514	1	US-07-872-644-17
11	1636.5	61.2	514	1	US-08-297-494-17
12	1636.5	61.2	514	1	US-08-297-510-17
13	1636.5	61.2	514	1	US-08-479-532-17
14	1636.5	61.2	514	1	US-08-455-526-17
15	1636.5	61.2	514	1	US-08-455-525-17
16	1636.5	61.2	514	3	US-09-139-491-17
17	1636.5	61.2	514	5	PCT-US92-03222-17
18	1593	59.5	634	1	US-07-872-644-51
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20	1593	59.5	634	1	US-08-297-510-51
21	1593	59.5	634	1	US-08-479-532-51
22	1593	59.5	634	1	US-08-455-526-51
23	1593	59.5	634	1	US-08-455-525-51
24	1593	59.5	634	3	US-09-139-491-51
25	1593	59.5	634	5	PCT-US92-03222-51
26	1591.5	59.5	530	1	US-07-872-644-6
27	1591.5	59.5	530	1	US-08-297-494-6

28	1591.5	59.5	530	1	US-08-297-510-6	Sequence 6, Appl1
29	1591.5	59.5	530	1	US-08-479-532-6	Sequence 6, Appl1
30	1591.5	59.5	530	1	US-08-455-526-6	Sequence 6, Appl1
31	1591.5	59.5	530	1	US-08-455-525-6	Sequence 6, Appl1
32	1591.5	59.5	530	3	US-09-139-491-6	Sequence 6, Appl1
33	1591.5	59.5	530	5	PCT-US92-03222-6	Sequence 6, Appl1
34	1568.5	58.6	535	1	US-07-872-644-49	Sequence 49, Appl
35	1568.5	58.6	535	1	US-08-297-494-49	Sequence 49, Appl
36	1568.5	58.6	535	1	US-08-297-510-49	Sequence 49, Appl
37	1568.5	58.6	535	1	US-08-479-532-49	Sequence 49, Appl
38	1568.5	58.6	535	1	US-08-455-526-49	Sequence 49, Appl
39	1568.5	58.6	535	3	US-09-139-491-49	Sequence 49, Appl
40	1568.5	58.6	535	5	PCT-US92-03222-49	Sequence 49, Appl
41	1568.5	58.6	535	5	PCT-US92-03222-49	Sequence 49, Appl
42	1206	45.1	564	1	US-07-872-644-53	Sequence 53, Appl
43	1206	45.1	564	1	US-08-297-494-53	Sequence 53, Appl
44	1206	45.1	564	1	US-08-297-510-53	Sequence 53, Appl
45	1206	45.1	564	1	US-08-479-532-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1  
US-08-940-332-2  
; Sequence 2, Application US/08940332  
; Patent No. 5885834  
; GENERAL INFORMATION:  
; APPLICANT: Epstein, Paul M.  
; TITLE OF INVENTION: SYNTHESIS OF ANTISENSE  
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE OF PHOSPHODIESTERASE AND  
; TITLE OF INVENTION: INDUCEMENT OF APOPTOSIS IN HUMAN LYMPHOBLASTOID CELLS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ALIX, YALE & RISTAS, LLP  
; STREET: 750 MAIN STREET  
; CITY: HARTFORD  
; STATE: CT  
; COUNTRY: USA  
; ZIP: 06103-2721  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/940,332  
; FILING DATE: 30-SEP-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,207  
; FILING DATE: 30-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Alix, James E.  
; REGISTRATION NUMBER: 20,736  
; REFERENCE/DOCKET NUMBER: UCON/137/US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (860)527-9211  
; TELEFAX: (860)527-5029  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 536 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-940-332-2

Query Match 96.5%; Score 2582; DB 2; Length 536;  
Best Local Similarity 100.0%; Pred. No. 1.3e-244;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 19 LRYMKQLNGEINTEELKKNLEYTASLEAVYIDETROIILDTDELQELRSDAVPSEVR 78  
DB 39 LRYMKQLNGEINTEELKKNLEYTASLEAVYIDETROIILDTDELQELRSDAVPSEVR 98

QY 79 DWLASTTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPTYSTAVLNCL 138  
DB 99 DWLASTTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPTYSTAVLNCL 158  
QY 139 KNLDFWCFDVSFLNQADDDHALRTIVFELLTRHNLISREKIPFVFLMSFLDALETGYGKY 198  
DB 159 KNLDFWCFDVSFLNQADDDHALRTIVFELLTRHNLISREKIPFVFLMSFLDALETGYGKY 218  
QY 199 KNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAHHDYEHTGTTNSPHIQ 258  
DB 219 KNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAHHDYEHTGTTNSPHIQ 278  
QY 259 KSECAIYVNDRSVLENHHSVFLMDDDMNIFINLTDEFFELRALVIEMLATDMSC 318  
DB 279 KSECAIYVNDRSVLENHHSVFLMDDDMNIFINLTDEFFELRALVIEMLATDMSC 338  
QY 319 HFQOVKTMKALQOLERIDPKKALSLLHHAADISHPTKQWLHVSRTWKALMEEFFRQGD 378  
DB 339 HFQOVKTMKALQOLERIDPKKALSLLHHAADISHPTKQWLHVSRTWKALMEEFFRQGD 398  
QY 379 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSQVQPLADEDSKSNQP 438  
DB 399 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSQVQPLADEDSKSNQP 458  
QY 439 SFQWRQPSLDVEGDPNDPVVSRSTWVKRIQENKQWKERRAASGITNQMIDELSPCEE 498  
DB 459 SFQWRQPSLDVEGDPNDPVVSRSTWVKRIQENKQWKERRAASGITNQMIDELSPCEE 518  
QY 499 EAPPSPAEDEHNGNGLD 516  
DB 519 EAPPSPAEDEHNGNGLD 536

## RESULT 2

US-07-872-644-27 Application US/07872644  
Sequence 27, Patent No. 5389527

## GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/872,644  
FILING DATE: 19920420  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5389527 and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 534 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-872-644-27

Query Match 92.88; Score 2484.5; DB 1; Length 534;

Best Local Similarity 96.08; Pred. No. 4.9e-235;

Matches 476; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 19 LRYWVQLENGEINIEELKNLEYTASLLAEVYIDETROQLDTEDELOELRSDAVPSEVR 78

DB 38 LRYWVQLENGEINIEELKNLEYTASLLAEVYIDETROQLDTEDELOELRSDAVPSEVR 97

QY 79 DWLASTTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPTYSTAVLNCL 138

DB 98 DWLASTTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPTYSTAVLNCL 156

QY 139 KNLDFWCFDVSFLNQADDDHALRTIVFELLTRHNLISREKIPFVFLMSFLDALETGYGKY 198

DB 157 KNLDFWCFDVSFLNQADDDHALRTIVFELLTRHNLISREKIPFVFLMSFLDALETGYGKY 216

QY 199 KNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAHHDYEHTGTTNSPHIQ 258

DB 217 KNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAHHDYEHTGTTNSPHIQ 276

QY 259 KSECAIYVNDRSVLENHHSVFLMDDDMNIFINLTDEFFELRALVIEMLATDMSC 318

DB 277 KSECAIYVNDRSVLENHHSVFLMDDDMNIFINLTDEFFELRALVIEMLATDMSC 336

QY 319 HFQOVKTMKALQOLERIDPKKALSLLHHAADISHPTKQWLHVSRTWKALMEEFFRQGD 378

DB 337 HFQOVKTMKALQOLERIDPKKALSLLHHAADISHPTKQWLHVSRTWKALMEEFFRQGD 396

QY 379 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSQVQPLADEDSKSNQP 438

DB 397 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSQVQPLADEDSKSNQP 456

QY 439 SFQWRQPSLDVEGDPNDPVVSRSTWVKRIQENKQWKERRAASGITNQMIDELSPCEE 498

DB 457 SFQWRQPSLDVEGDPNDPVVSRSTWVKRIQENKQWKERRAASGITNQMIDELSPCEE 516

QY 499 EAPPSPAEDEHNGNGLD 516

DB 517 EAPPSPAEDEHNGNGLD 534

## RESULT 3

US-08-297-494-27

Sequence 27, Application US/08297494

Patent No. 5580771

GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.

APPLICANT: Bentley, Kelley

APPLICANT: Charbonneau, Harry

APPLICANT: Sonnenburg, William K.

TITLE OF INVENTION: DNA Encoding Mammalian

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp;

ADDRESSEE: Bicknell

STREET: Two First National Plaza, 20 South Clark

STREET: Street

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,494  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NO. 558071and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-297-494-27

Query Match 92.8%; Score 2484.5; DB 1; Length 534;  
Best Local Similarity 96.0%; Pred. No. 4.9e-235;  
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;  
QY 19 LRYMYKQLENGEINTEELKKNLEYTASLLEAVYIDETROIILDEBELQELRSDAVPSEVR 78  
DB 38 LRYMYKQLENGEVNTEELKKNLEYTASLLEAVYIDETROIILDEBELQELRSDAVPSEVR 97  
QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERFMFRRTYTSVGPITYSTAVLNCL 138  
DB 98 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERFMFRRTYTSVGPITYSTAVLNCL 156  
QY 139 KNDLWCFDVSINQAADHALRTIVFELLTRHNLISRPKIPTVFLMFLDALETGYGKY 198  
DB 157 KNDLWCFDVSINQAADHALRTIVFELLTRHNLISRPKIPTVFLMFLDALETGYGKY 216  
QY 199 KNPYHNQIHAADVTQVHCFLRTGMVHCLSEIELLAIIFAAAIHDYHTGTNSPHIQT 258  
DB 217 KNPYHNQIHAADVTQVHCFLRTGMVHCLSEIELLAIIFAAAIHDYHTGTNSPHIQT 276  
QY 259 KSECAIVYNDRSVLENHHISSVFRMLQDDMMNIFNLTKDEFVELRALVIEVMTATDMSK 318  
DB 277 KSECAIVYNDRSVLENHHISSVFRMLQDDMMNIFNLTKDEFVELRALVIEVMTATDMSK 336  
QY 319 HFQOQVTKMTALQQLERIDKPKALSLLHAADISHPTKQWLVSRTWKALMEEFRRQGDK 378  
DB 337 HFQOQVTKMTALQQLERIDKPKALSLLHAADISHPTKQWLVSRTWKALMEEFRRQGDK 396  
QY 379 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKKNQP 438  
DB 397 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKKNQP 456  
QY 439 SFQWRQPSLDVGPDPNPDVFRSTWVKRIQENKQKERAASGITTNQMSIDELSPCEE 498  
DB 457 SFQWRQPSLDVGPDPNPDVFRSTWVKRIQENKQKERAASGITTNQMSIDELSPCEE 516  
QY 499 EAPSPAEDHQNQNL 516  
DB 517 EAPSPAEDHQNQNL 534

RESULT 4

US-08-297-510-27  
; Sequence 27, Application US/08297510  
; Patent No. 5602019  
; GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Bicknell,  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,510  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NO. 5602019and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-297-510-27

Query Match 92.8%; Score 2484.5; DB 1; Length 534;  
Best Local Similarity 96.0%; Pred. No. 4.9e-235;  
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;  
QY 19 LRYMYKQLENGEINTEELKKNLEYTASLLEAVYIDETROIILDEBELQELRSDAVPSEVR 78  
DB 38 LRYMYKQLENGEVNTEELKKNLEYTASLLEAVYIDETROIILDEBELQELRSDAVPSEVR 97  
QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERFMFRRTYTSVGPITYSTAVLNCL 138  
DB 98 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERFMFRRTYTSVGPITYSTAVLNCL 156  
QY 139 KNDLWCFDVSINQAADHALRTIVFELLTRHNLISRPKIPTVFLMFLDALETGYGKY 198  
DB 157 KNDLWCFDVSINQAADHALRTIVFELLTRHNLISRPKIPTVFLMFLDALETGYGKY 216  
QY 199 KNPYHNQIHAADVTQVHCFLRTGMVHCLSEIELLAIIFAAAIHDYHTGTNSPHIQT 258  
DB 217 KNPYHNQIHAADVTQVHCFLRTGMVHCLSEIELLAIIFAAAIHDYHTGTNSPHIQT 276  
QY 259 KSECAIVYNDRSVLENHHISSVFRMLQDDMMNIFNLTKDEFVELRALVIEVMTATDMSK 318  
DB 277 KSECAIVYNDRSVLENHHISSVFRMLQDDMMNIFNLTKDEFVELRALVIEVMTATDMSK 336  
QY 319 HFQOQVTKMTALQQLERIDKPKALSLLHAADISHPTKQWLVSRTWKALMEEFRRQGDK 378  
DB 337 HFQOQVTKMTALQQLERIDKPKALSLLHAADISHPTKQWLVSRTWKALMEEFRRQGDK 396  
QY 379 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKKNQP 438





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;       TELEX: 25-3856
;       INFORMATION FOR SEQ ID NO
;       SEQUENCE CHARACTERISTICS
;       LENGTH: 534 amino ac
;       TYPE: amino acid
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-455,526-27

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Query Match	92.98;	Score	2484.5;	DB 1;	Length	534;			
Best Local Similarity	96.0%;	Pred. No.	4.9e-235;						
Matches	478;	Conservative	10;	Mismatches	9;	Indels	1;	Gaps	1;
QY	19	LRVWVQLNGEINIELKKNLEVTASLLAEAVYIDETQRLDTEDEQLQELSDVAPSEVR	78						
Db	38	LRVWVQLNGEVNIELKKNLEVTASLLAEAVYIDETQRLDTEDEQLQELSDVAPSEVR	97						
QY	79	DWLASTFTQARAKRAAEKPKFRSIVHAVQAGIFVERMFRRTYTSVGPITYSTAVLNCL	138						
Db	98	DWLASTFTQTRAKG-PSEKPKFRSIVHAVQAGIFVERMFRRTYTSVGPITYSTAVLNCL	156						
QY	139	KNLDLKCDFVSLNQAADHIALRTIVPELLTRHNLSIRFKIPYVFLMSFLDALSTGYGY	198						
Db	157	KNYDLKCFDFSLNRAADHIALRTIVPELLTRHNLSIRFKIPTVFLMTFLDALETGYGY	216						
QY	199	KNPYHNOIHAADVTQTVHCFLRTGMVHCISETELLAIFAAATHDYEHTGTTNSFHIQT	258						
Db	217	KNPYHNOIHAADVTQTVHCFLRTGMVHCISETEVLAIIFAAATHDYEHTGTTNSFHIQT	276						
QY	259	KSECAIYNDRSVLENNHISVSFRMLQDDMNFINLTQDFVELRALVIEMLVATDMSC	318						
Db	277	KSECAIYNDRSVLENNHISVSFRMQDDMNFINLTQDFVELRALVIEMLVATDMSC	336						
QY	319	HFQOQVMTKALQOLERIDKPKALLSLLHAADISHPTQKWLVHSRWTKALMEEFPROGDK	378						
Db	337	HFQOQVSMKTALQOLERIDKSKALLSLLHAADISHPTQKQSVHSRWTKALMEEFPROGDK	396						
QY	379	EAEGLGPFSPCLDRTSTLVAQSIGFTDFIVEPTFSVLTDVAEKSQVPLADEDSKKNQP	438						
Db	397	EAEGLGPFSPCLDRTSTLVAQSIGFTDFIVEPTFSVLTDVAEKSQVPTGDDDSKKNQP	456						
QY	439	SFQWRQPSLDVEVDGPNPDVVSFRSTWVKRIQENKQKWKERRAASGINQMSIDELSPCEE	498						
Db	457	SFQWRQPSLDVEVDGPNPDVVSFRSTWTKYIQENKQKWKERRAASGINQMSIDELSPCEE	516						
QY	499	EAPSPAEDHNGNGLD	516						
Db	517	EAPSPAEDHNGNGLD	534						

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RESULT 7
US-08-455-525-27
; Sequence 27, Application US/08455525
; Patent No. 5800987
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K
; TITLE OF INVENTION: DNA Encoding
; TITLE OF INVENTION: Phosphodiester
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole,
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,525
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5800987and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-455-525-27

Query Match 92.88; Score 2484.5; DB 1; Length 534;
Best Local Similarity 96.0%; Pred. No. 4.9e-235;
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 19 LRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETROI LDTDELEQLRSDAVPSEVR 78
Db 38 LRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETROI LDTDELEQLRSDAVPSEVR 97
QY 79 DWLASTFTQOARAKGRRAEKKPFRSIVHAVAQAGIFVERMFRRTYTSVGPTYSTAVLNCL 138
Db 98 DWLASTFTQOAKRG-PSEKKPFRSIVHAVAQAGIFVERMFRRTYTSVGPTYSTAVLNCL 156
QY 139 KNYDLWCDFVSLNQAADHALRTIVFELLTRNLNLSRFPKIPTVFLMSFLDALETGYGKY 198
Db 157 KNYDLWCDFVSLNRAADHALRTIVFELLTRNLNLSRFPKIPTVFLMTFLDALETGYGKY 216
QY 199 KNPYHNQIHAADVTQVHVCFLLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSPHIQ 258
Db 217 KNPYHNQIHAADVTQVHVCFLLRTGMVHCLSEIEVLAIIFAAAIHDYEHGTGTTNSPHIQ 276
QY 259 KSECAIYVNDRSVLENNHIISSVPRLMQDDSENNIFINLTDKDEFVELRALVIEMVLATDMSC 318
Db 277 KSECAIYVNDRSVLENNHIISSVPRFMQDDSENNIFINLTDKDEFVELRALVIEMVLATDMSC 336
QY 319 HFQOQVTKMTALQOLERIDKPKALSLLLHAADISHPTKQMLVHSRWTKALMEEFFRQGDK 378
Db 337 HFQOQVSKMTALQOLERIDKSKALSLLLHAADISHPTKQWSVHSRWTKALMEEFFRQGDK 396
QY 379 EABLGLPFPSPCLDRTSTLVAQSOIGFTDFTEVETFSVLTDVAEKSVQPLADEDSKKNQP 438
Db 397 EABLGLPFPSPCLDRTSTLVAQSOIGFTDFTEVETFSVLTDVAEKSVQPTGDDDSKKNQP 456
QY 439 SFQWRQPSLDVEGDPNDPVVSPRSTWVKRQENKQKWKRAAASGITNQMISIDELSPCEE 498
Db 457 SFQWRQPSLDVEGDPNDPVVSPRSTWTKYIQENKQKWKRAAASGITNQMISIDELSPCEE 516
QY 499 EAPPPSPAEDHNQNGNLD 516
Db 517 EAPASPAEDHNQNGNLD 534

RESULT 8
US-09-139-491-27
; Sequence 27, Application US/09139491
; Patent No. 6015677

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GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/139,491  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,525  
FILING DATE: 31-MAY-1995  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 601567/and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-03222-27

Query Match 92.8%; Score 2484.5; DB 3; Length 534;  
Best Local Similarity 96.0%; Pred. No. 4.9e-235;  
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;  
QY 19 LRYMKVQLNGEINIEELKKNLEYTASLLEAVYIDETROIILDELOELRSDAVPSEVR 78  
DB 38 LRYMKVQLNGEINIEELKKNLEYTASLLEAVYIDETROIILDELOELRSDAVPSEVR 97  
QY 79 DWLASTTQOAKRGRABEKPFRSIVHVAQGFVERMFRRTYTSVGTYSTAVLNCL 138  
DB 98 DWLASTTQOAKRGRABEKPFRSIVHVAQGFVERMFRRTYTSVGTYSTAVLNCL 156  
QY 139 KNDLMCFDVFSLNQADHALRTIVFELLTRHNLISREKIPTVFLMSFLDALETGYGKY 198  
DB 157 KNDLMCFDVFSLNQADHALRTIVFELLTRHNLISREKIPTVFLMSFLDALETGYGKY 216  
QY 199 KNPYHNQIHAADVOTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYHTGTTNSFHIOT 258  
DB 217 KNPYHNQIHAADVOTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYHTGTTNSFHIOT 276  
QY 259 KSECAIVNDRSVLENHHISSVFRMLQDDMMNIFNLTKDEFVELRALVIENVLATDMSC 318  
DB 277 KSECAIVNDRSVLENHHISSVFRMLQDDMMNIFNLTKDEFVELRALVIENVLATDMSC 336

QY 319 HFQOVYTKMTALQOOLERIDKPKALSLLHAAADISHPTKOWLVHSRWTKALMEEFFROGDK 378  
DB 337 HFQOVYTKMTALQOOLERIDKPKALSLLHAAADISHPTKOWLVHSRWTKALMEEFFROGDK 396  
QY 379 EAEGLGPFSPCLCDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVOPLADEDSKSNQP 438  
DB 397 EAEGLGPFSPCLCDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVOPTDGDDSKSNQP 456  
QY 439 SFQWRQPSLDVEVGDPNDPVVSRSTWVKRIQENKOKWKERAAAGITNQMSIDELSPCEE 498  
DB 457 SFQWRQPSLDVEVGDPNDPVVSRSTWVKRIQENKOKWKERAAAGITNQMSIDELSPCEE 516  
QY 499 EAPPSPAEDHNONGNLD 516  
DB 517 EAPPSPAEDHNONGNLD 534  
RESULT 9  
PCT-US92-03222-27  
Sequence 27, Application PC/TUS9203222  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/03222  
FILING DATE: 19920420  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-03222-27  
Query Match 92.8%; Score 2484.5; DB 5; Length 534;  
Best Local Similarity 96.0%; Pred. No. 4.9e-235;  
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;  
QY 19 LRYMKVQLNGEINIEELKKNLEYTASLLEAVYIDETROIILDELOELRSDAVPSEVR 78  
DB 38 LRYMKVQLNGEINIEELKKNLEYTASLLEAVYIDETROIILDELOELRSDAVPSEVR 97

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QY 79 DMLASTFTQARAKGRABEKPFRSIVHVAQIGFVERFMFRRTYSVGTYSTAVLNCL 138
Db 98 DMLASTFTQTRAKG-PSEKPKFRSIVHVAQIGFVERFMFRRTYSVGTYSTAVLNCL 156
QY 139 KNDLWCFDVSINQAADHALRTIVFELLTRHNLISREKPIPTVFLMSFLDALETGYKY 198
Db 157 KNVDLWCFDVSINRAADHALRTIVFELLTRHNLISREKPIPTVFLMTFLDALETGYKY 216
QY 199 KNPYHNOIHAADVTQVHCFLLRTGMVHCLSETELLAIIFAAAIHDIHYEHTGNTNSPHIOT 258
Db 217 KNPYHNOIHAADVTQVHCFLLRTGMVHCLSETELLAIIFAAAIHDIHYEHTGNTNSPHIOT 276
QY 259 KSECAIYVNDRSVLENHHSVFLRMQDDMMIFINLTKDEFVELRALVIEMVLATDMSC 318
Db 277 KSECAIYVNDRSVLENHHSVFLRMQDDMMIFINLTKDEFVELRALVIEMVLATDMSC 336
QY 319 HFQOVKMTALQQLERIDKPKALSLLHAADISHTPKOWLHSHRWTKALMEEFFRQGD 378
Db 337 HFQOVKSMKTALQQLERIDKPKALSLLHAADISHTPKOWSHRWTKALMEEFFRQGD 396
QY 379 EAEGLPFPPLCDRTSTLVAQSIGFIDFIVEPTESVLTDAEKSVOPLADEDSKSNOP 438
Db 397 EAEGLPFPPLCDRTSTLVAQSIGFIDFIVEPTESVLTDAEKSVOPTGDDDSKSNOP 456
QY 439 SFQWRQPSLDEVGDPNDPVFSFRSTWVKRIQENKOKKERAASGITNOMSIDELSPCEE 498
Db 457 SFQWRQPSLDEVGDPNDPVFSFRSTWVKRIQENKOKKERAASGITNOMSIDELSPCEE 516
QY 499 EAPPSAEDHONGNLD 516
Db 517 EAPPSAEDHONGNLD 534

RESULT 10
US-07-872-644-17
; Sequence 17, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,644
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5389527and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
```

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; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-872-644-17

Query Match 61.2%; Score 1636.5; DB 1; Length 514;
Best Local Similarity 60.8%; Pred. No. 7.2e-152;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

QY 1 MANPVPQVSHLQGPILRLRYMYKQLENGEINTEELKKNLKYFASLEAVYIDETQILD 60
Db 1 MDHVTIRKHLQRPFRKLCLVKQLEKGVNVIDLKKIEYAASVLEAVYIDETRLLD 60
QY 61 TEDELQELSDAVPSEVRDMLASTFTQAKARAKGRABEKPFRSIVHVAQIGFVERMFR 120
Db 61 TDELSDIQSDSVSEVRDMLASTFTRKMGMMKKKSEKPRPRRSIVHVQAGIFVERMYR 120
QY 121 RYTSVGPYSTAVLNCLNLDLWCFDVSINQAADHALRTIVFELLTRHNLISREKPI 180
Db 121 KSYHMYGLAYPEAVIIVTLKDVKWSDFVFNALNEASGEHSLKFMIELFTRYDLINRKIP 180
QY 181 TVFLMSFLDALETGYGKYKNPNYHNOIHAADVTQVHCFLLRTGMVHCLSETELLAIIFAA 240
Db 181 VSLIAFAEALEVGYSKYKNPNYHNOIHAADVTQVHYIMLHTGIMHMLTELEILAMVFAA 240
QY 241 AIHDYEHTGTTNSFHITQKSECAIYVNDRSVLENHHSVFLRMQDDMMIFINLTQDEF 300
Db 241 AIHDYEHTGTTNNFHITQKSDVAILYNDRSVLENHHSVAAAYRLMQEEMNLNLSKDDW 300
QY 301 VELRALVIEVLATDMSCHFQOVKMTALQQLERIDKPKALSLLHAADISHTPKOWL 360
Db 301 RDLNLVIEVLATDMSCGHFQOVKMTALQQLERIDKPKALSLLHAADISHTPKOWL 360
QY 361 HSRWTKALMEEFFRQGDKEALGLPFPPLCDRTSTLVAQSIGFIDFIVEPTESVLTDA 420
Db 361 HSRWTKALMEEFFRQGDKEALGLPFPPLCDRTSTLVAQSIGFIDFIVEPTESVLTDA 420
QY 421 EKSQVPLADEDSKSNOPSFQWRQPSLDEVGDP-----PNPDVVSFRSTWVKRIQE 471
Db 421 EKIIIPLEEDSKTKTPSYGASRRSNMKGTTNDGTVSPDYSLASVDLKSFKNSLVDIIQ 480
QY 472 NKQWKERAASGITNOMSIDELSPCEE 499
Db 481 NKERWKEAQAQGPDPHKNKNSDLVNAEEK 508

RESULT 11
US-08-297-494-17
; Sequence 17, Application US/08297494
; Patent No. 5580771
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; - APPLICATION NUMBER: US/08/297,494
; - FILING DATE:
; - CLASSIFICATION: 435
; - PRIOR APPLICATION DATA:
; - APPLICATION NUMBER: US 07/688,356
; - FILING DATE: 04-APR-1991
; - ATTORNEY/AGENT INFORMATION:
; - NAME: NO. 558077land, Greta E.
; - REGISTRATION NUMBER: 35,302
; - REFERENCE/DOCKET NUMBER: 27866/30822
; - TELECOMMUNICATION INFORMATION:
; - TELEPHONE: (312) 346-5750
; - TELEFAX: (312) 984-9740
; - TELEX: 25-3856
; - INFORMATION FOR SEQ ID NO: 17:
; - SEQUENCE CHARACTERISTICS:
; - LENGTH: 514 amino acids
; - TYPE: amino acid
; - TOPOLOGY: linear
; - MOLECULE TYPE: protein
; US-08-297-494-17

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Query Match	61.2%	Score 1636.5	DB 1	Length 514
Best Local Similarity	60.8%	Pred. No. 7.2e-152		
Matches	Conservative 94	Mismatches 96	Indels 9	Gaps 1
QY	1	MANPVPQSRHGGPILRLRYWKQJLJENGSEINIEELKKNLEYTASLLEAVYIDETROI	LD	60
DB	1	MDDHVYIRRKHQQRIPFLRCLVYQLEKGDVNNIDLKKNTIEYAAASVLEAVYIDETRE	LLD	60
QY	61	TEDELOELSDAVPSEVDMVLASTFTQQARAKARRAEKPKFRSIHAVQAQGFVERMFR		120
DB	61	TDDELDSDIQSDSPSEVDMVLASTFTKMGMMKKSEKPKFRSIHVHQAQGFVERMYR		120
QY	121	RTVSYGPPYSTAVLNCNLKLDLWCDFVDSFNQAADDHALRTIVFELLTRHNLISRKPI		180
DB	121	KSYHVMGLAYPEAVITVLKDVKDSFDFALNEASGEHSLKFUYELFTRYDITNRKPI		180
QY	181	TVFLMSFLDALETGYGKYKNPYINQIHAADVDTQVCHLLRTGMVHCLSEIELALIFAA		240
DB	181	VSLCIAFAEALEVGYSKYKNPYINLHAADVDTQVHYIMLHTGIMHMLWTELEILAMVFA		240
QY	241	AIDHYEHTGTNSFHJQTKSECAIVYNDRSVLNHHIISVFLMQDDMMFINLTKDEF		300
DB	241	AIDHYEHTGTNNFHTQTRSDVAILYNDRSVLNHHVSAAYRLMQEEMVNLNLSKDDW		300
QY	301	VELRALVIEMLVATDMSCHFQVYKTKALQQLERIDKPKALSLILHAADISHPTKOWLV		360
DB	301	RDRLNVLVIEMLVTDMSGHFQQIKNTRNSLQPEGLDKAKTMSLILHAADISHPAKSWKL		360
QY	361	HSRWTALMBEFPQGDKAELGPTSPICDRTSTLVAQSIGIFDIVEPFTSVLTDVA		420
DB	361	HRHWTALMBEFPLOQDKAELGPTSPICDRKSTWVAQSIGIFDIVEPFTSLLYDST		420
QY	421	EKSQVPLADEDSKSNQPSFQWRQPSLDLVEVGQ-----PNPDVVSPRSTWVKRIQE		471
DB	421	EKKIILPLIEDSKTSPYCGASRRSNKGTINDGTSPDYSLASVDLKSFKNSLDVLIQ		480
QY	472	NKQKWKERAASGITNOMSIDELSPCEEE		499
DB	481	NKRWKELAAQGEPPDKHNSDLVNAEEK		508

RESULT 12

RESOL 12  
US-08-297-510-17  
; Sequence 17, Application US/08297510  
; Patent No. 5602019  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.

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Db 361 HHRWTMALMEEFFLOGDKEAELGLPSPLCDRKSTWVAQSIGFIDFIVEPTFSLTDTST 420
Qy 421 EKSVOPLADEDSKSNQPSFQWRQPSLDVEVGD-----PNDVVSFSTWVKRQOE 471
Db 421 EKIIIPLEEDSKTKTPSYGASRRSNMKGTTNDGTYSPTYSLASVDLAKSFKNLSLDIQQ 480
Qy 472 NKQWKERAASGITNOMSIDELSPCEEE 499
Db 481 NKERWELAAOGEPPDPHKNLSLDVNAEEK 508

RESULT 13
US-08-479-532-17
; Sequence 17, Application US/08479532
; Patent No. 5776752
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,532
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5776752and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-532-17

Query Match 61.2%; Score 1636.5; DB 1; Length 514;
Best Local Similarity 60.8%; Pred. No. 7.2e-152;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

Qy 1 MANPVQSLQGPILRLYVMVKOLENGEINIELKKNLEYTASLLBAVYIDETFRQLD 60
Db 1 MDDHTYIRKHLQRFIFRLCLVQLEKGDVNDLKKNIETAAVSLVAVYIDETFRRLD 60
Qy 61 TEDELQELRSDAVSEVRDLASTFTQARAKGRAEKKPRFSIVHVAQAGIFVERMFR 120
Db 61 TDDELSDIQSDSVSEVRDLASTFTTRKGMWKKSEKPRFSIVHVVQAGIFVERMYR 120
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INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 514 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-455-526-17

Query Match 61.2%; Score 1636.5; DB 1; Length 514;  
Best Local Similarity 60.8%; Pred. No. 7.2e-152;  
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

QY 1 MANPVQSHLQGLRLRYMVKOLENGEINIEELKKNLEYTASLEAVYIDETRIQLD 60  
Db 1 MDDHVTIRKKHLQRIPLRCLVKOLEKGVNVDLKNIEYAASVLEAVYIDETRIQLD 60  
QY 61 TEDELQELSDAVPSEVRDLASTFTQQAARAKGRRAEKKPKFRSIVHAYVQAGIFVERMYR 120  
Db 61 TDELSDIQSDSPSEVRDLASTFTQQAARAKGRRAEKKPKFRSIVHAYVQAGIFVERMYR 120  
QY 121 RYTSVGYPTYSTAVLNCLNLDLWCFVSLNQAADHALRTIVFELLTRHNLISRFKIP 180  
Db 121 KSYHVMGLAYPEAVITLKDVKWDFVFNALNEASGEHSLKPMIYELFTRYDLINRFKIP 180  
QY 181 TVFLMSFLDALEFGYGYKKNPYHNOIHAADVTQTVHCLRTGMVHCLSEIELLAIIFAA 240  
Db 181 VSLIAFAEALEFGYGYKKNPYHNLIIHAADVTQTVHCLRTGMVHCLSEIELLAIIFAA 240  
QY 241 AIHDYEHTGTTNSPHIOTKSECAIVYNDRSVLENHHISSVFLRMQDDENFINLTKDEF 300  
Db 241 AIHDYEHTGTTNPHIOTKSECAIVYNDRSVLENHHISSVFLRMQDDENFINLTKDEF 300  
QY 301 VELRALVIEVLATDMSCHFOQVTKMTALQOLERIDPKALSLHAAADISHPTKQWLV 360  
Db 301 RDLRLVIEVLATDMSCHFOQVTKMTALQOLERIDPKALSLHAAADISHPTKQWLV 360  
QY 361 HSRWTKALMEEFPRQGDKEAELGLPSPICDRTSTLVAOSQIGFIDFIVEPTFSLTDT 420  
Db 361 HHRWTALMEEFPRQGDKEAELGLPSPICDRTSTLVAOSQIGFIDFIVEPTFSLTDT 420  
QY 421 EKSQVPLADEDSKKNQPSFQWRQPSLDVEVGD-----PNPDVVSFRSTWVKRQOE 471  
Db 421 EKIIPLIEEDSKTKTPSYGASRRSNMKGTTNDGTYSPTYSLASVDLKSFKNSLVDIIQQ 480

RESULT 15  
US-08-455-525-17  
Sequence 17, Application US/08455525  
Patent No. 5800987

GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,525  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NO. 5800987 and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 514 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-455-525-17

Query Match 61.2%; Score 1636.5; DB 1; Length 514;  
Best Local Similarity 60.8%; Pred. No. 7.2e-152;  
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

QY 1 MANPVQSHLQGLRLRYMVKOLENGEINIEELKKNLEYTASLEAVYIDETRIQLD 60  
Db 1 MDDHVTIRKKHLQRIPLRCLVKOLEKGVNVDLKNIEYAASVLEAVYIDETRIQLD 60  
QY 61 TEDELQELSDAVPSEVRDLASTFTQQAARAKGRRAEKKPKFRSIVHAYVQAGIFVERMYR 120  
Db 61 TDELSDIQSDSPSEVRDLASTFTQQAARAKGRRAEKKPKFRSIVHAYVQAGIFVERMYR 120  
QY 121 RYTSVGYPTYSTAVLNCLNLDLWCFVSLNQAADHALRTIVFELLTRHNLISRFKIP 180  
Db 121 KSYHVMGLAYPEAVITLKDVKWDFVFNALNEASGEHSLKPMIYELFTRYDLINRFKIP 180  
QY 181 TVFLMSFLDALEFGYGYKKNPYHNOIHAADVTQTVHCLRTGMVHCLSEIELLAIIFAA 240  
Db 181 VSLIAFAEALEFGYGYKKNPYHNLIIHAADVTQTVHCLRTGMVHCLSEIELLAIIFAA 240  
QY 241 AIHDYEHTGTTNSPHIOTKSECAIVYNDRSVLENHHISSVFLRMQDDENFINLTKDEF 300  
Db 241 AIHDYEHTGTTNPHIOTKSECAIVYNDRSVLENHHISSVFLRMQDDENFINLTKDEF 300  
QY 301 VELRALVIEVLATDMSCHFOQVTKMTALQOLERIDPKALSLHAAADISHPTKQWLV 360  
Db 301 RDLRLVIEVLATDMSCHFOQVTKMTALQOLERIDPKALSLHAAADISHPTKQWLV 360  
QY 361 HSRWTKALMEEFPRQGDKEAELGLPSPICDRTSTLVAOSQIGFIDFIVEPTFSLTDT 420  
Db 361 HHRWTALMEEFPRQGDKEAELGLPSPICDRTSTLVAOSQIGFIDFIVEPTFSLTDT 420  
QY 421 EKSQVPLADEDSKKNQPSFQWRQPSLDVEVGD-----PNPDVVSFRSTWVKRQOE 471  
Db 421 EKIIPLIEEDSKTKTPSYGASRRSNMKGTTNDGTYSPTYSLASVDLKSFKNSLVDIIQQ 480

Search completed: August 11, 2003, 01:13:38  
Job time : 45 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2003, 01:11:57 ; Search time 337 Seconds  
(without alignments)  
181.840 Million cell updates/sec

Title: US-09-663-481-1

Perfect score: 2676

Sequence: 1 MANPVPQSRHLQPIILRLR.....EEEAAPPSPAEHNGNGLD 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2484.5	92.8	534	10	US-09-883-825-27
2	1636.5	61.2	514	10	US-09-883-825-17
3	1593	59.5	634	10	US-09-883-825-51
4	1591.5	59.5	530	10	US-09-883-825-6
5	1568.5	58.6	535	10	US-09-883-825-49
6	1206	48.1	564	10	US-09-883-825-53
7	668	25.0	137	10	US-09-883-825-23
8	626	23.4	712	15	US-10-076-597-47
9	622.5	23.3	585	15	US-10-076-514-9
10	617.5	23.1	507	15	US-10-076-597-49
11	617.5	23.1	507	15	US-10-067-514-10
12	617.5	23.1	673	15	US-10-076-597-51
13	617.5	23.1	673	15	US-10-067-514-6
14	617.5	23.1	687	15	US-10-067-514-8
15	617.5	23.1	745	15	US-10-076-597-50

16	617.5	23.1	745	15	US-10-067-514-4
17	617.5	23.1	809	15	US-10-067-514-2
18	611.5	22.9	647	15	US-10-076-597-46
19	610.5	22.8	564	9	US-09-947-305-2
20	610.5	22.8	564	15	US-10-076-597-48
21	603.5	22.6	584	9	US-09-802-741A-4
22	461.5	17.3	426	11	US-09-966-781A-2
23	461.5	17.2	426	11	US-09-966-781A-3
24	457.5	17.1	426	11	US-09-966-781A-1
25	435.5	16.3	713	9	US-09-802-741A-3
26	435.5	15.8	432	9	US-09-764-898-208
27	405	15.1	580	15	US-10-083-620A-21
28	405	15.1	593	9	US-09-802-741A-1
29	403.5	15.1	533	15	US-10-083-620A-19
30	403	15.1	466	15	US-10-083-620A-2
31	390.5	14.6	320	15	US-10-083-620A-17
32	373.5	14.0	285	11	US-09-989-442-94
33	338	12.6	490	15	US-10-094-168B-1
34	338	12.6	576	10	US-09-891-216-13
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36	338	12.6	934	10	US-09-891-216-12
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38	336.5	12.6	905	14	US-10-094-989-4
39	336.5	12.6	920	14	US-10-094-989-2
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42	335.5	12.5	921	14	US-10-094-989-5
43	335.5	12.5	942	10	US-09-883-825-43
44	319.5	11.9	211	9	US-09-764-898-280
45	319.5	11.9	211	11	US-09-989-442-120

## ALIGNMENTS

### RESULT 1

US-09-883-825-27  
; Sequence 27, Application US/09883825  
; Patent No US20020151024A1

### GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.  
Bentley, Kelley  
Charbonneau, Harry  
Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bicknell  
STREET: Two First National Plaza, 20 South Clark Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/883,825  
FILING DATE: 18-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/123,783  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/297,494  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:

```

;
; NAME: No. US20020151024Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-883-825-27

Query Match 92.8%; Score 2484.5; DB 10; Length 534;
Best Local Similarity 96.0%; Pred. No. 7.5e-233;
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 19 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETQILDTDELEQLRSDAVPSEVR 78
Db 38 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETQILDTDELEQLRSDAVPSEVR 97
QY 79 DWLASTFTQARAKRAEKKPKRSIVHAVAQAGIFVERMFRRTYTSVGTPTYSTAVLNCL 138
Db 98 DWLASTFTQTRAKG-PSEKKPKRSIVHAVAQAGIFVERMFRRTYTSVGTPTYSTAVLNCL 156
QY 139 KNLDLWCDFVSLNQADDAHALRTIVFELLTRHNLISREFKIPTVFLMSFLDALETGYGY 198
Db 157 KNLDLWCDFVSLNRAADDAHALRTIVFELLTRHNLISREFKIPTVFLMFLDALETGYGY 216
QY 199 KNPYHNOIHAADVTQVHCFLLRTGMVHCLSELELLAIFAAAIHDEYHTGTTNSFHOT 258
Db 217 KNPYHNOIHAADVTQVHCFLLRTGMVHCLSELELLAIFAAAIHDEYHTGTTNSFHOT 276
QY 259 KSCAIVYNDRSVLENNHSSVFLRMQDDMMNIFINLTQDEFVELRALVIEVWLATDMS 318
Db 277 KSCAIVYNDRSVLENNHSSVFLRMQDDMMNIFINLTQDEFVELRALVIEVWLATDMS 336
QY 319 HFQOQVMTALQOLERIDKPKALSLLLHAADISHTPKOMLVHRSWTKALMBEFPQGD 378
Db 337 HFQOQVMTALQOLERIDKPKALSLLLHAADISHTPKOMLVHRSWTKALMBEFPQGD 396
QY 379 EAEGLGPFPLCDRTSTLVAQSQIGFIDFIVEPTFSLVDVAEKSVPQLADEDSKKNOP 438
Db 397 EAEGLGPFPLCDRTSTLVAQSQIGFIDFIVEPTFSLVDVAEKSVPQTDGDDSKKNOP 456
QY 439 SFQWRQPSLDVEGDPNPDVSPFRSTWVKRIQENKQKWKERAASGITNOMSIDELSPCEE 498
Db 457 SFQWRQPSLDVEGDPNPDVSPFRSTWTKYIOENKQKWKERAASGITNOMSIDELSPCEE 516
QY 499 EAPPSPAEDEHNGNLD 516
Db 517 EAPASPAEDEHNGNLD 534

RESULT 2
US-09-883-825-17
; Sequence 17, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
```

```

;
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-883-825-17

Query Match 61.2%; Score 1636.5; DB 10; Length 514;
Best Local Similarity 60.8%; Pred. No. 2.3e-150;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

QY 1 MANPYVORSHLQGPILRLRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETQIL 60
Db 1 MDHVTYIRKHLQRPFRRLCLVQLEKGDVNVIDLKKNIEYAASVLEAVYIDETRRLL 60
QY 61 TEDELQELRSDAVPSEVRDWLASTFTQARAKRAEKKPKRSIVHAVAQAGIFVERMFR 120
Db 61 TDELSLDSQSDVSPSEVRDWLASTFTRKMGMMKKSEKPKRSIVHVVQAGIFVERMYR 120
QY 121 RYTSVGTPTYSTAVLNCLNLDLWCDFVSLNQADDAHALRTIVFELLTRHNLISREFKI 180
Db 121 KSYHNVGLAYPEAVITVLKDVKWSFDVFNALNEASGEHSLRFMIYELTRYDLINRFKI 180
QY 181 TVFLMSFLDALETGYGYKNPYHNOIHAADVTQVHCFLLRTGMVHCLSELELLAIFAA 240
Db 181 VSLIRFAEALVEGYSKYNPYHNLHHAADVTQVHYIMLHTGIMHWTELELLAWFAA 240
QY 241 AIHDEYHTGTTNSFHOTKSECAIVYNDRSVLENNHSSVFLRMQDDMMNIFINLTQDEF 300
Db 241 AIHDEYHTGTTNNFHQTRSDVAILYNDRSVLENNHSSVFLRMQDDMMNVLINLSKDD 300
QY 301 VELRALVIEVWLATDMSCHFQOQVMTALQOLERIDKPKALSLLLHAADISHTPKQWL 360
Db 301 IDLRNLVIEVWLSTDMSGHFQOIKNIRNSLQOPEGLDKAKTMSLLHHAADISHPAKSN 360
QY 361 ISRWTKALMBEFPQGDKEAELGPFPLCDRTSTLVAQSQIGFIDFIVEPTFSLVDVA 420
Db 361 IHRWTMALMBEFPQGDKEAELGPFPLCDRTSTLVAQSQIGFIDFIVEPTFSLTDTST 420
QY 421 IKSVPQLADEDSKKNOPSFQWRQPSLDVEGDPNPDVSPFRSTWVKRIQENKQKWKERA 471
Db 421 IKIIPLEEDSKTKTPSYGASRRSNMKGTTNDGTYSYSLASVDLKSFKNSLVDIIQQ 480
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; INFORMATION FOR SEQ ID NO: 6
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6
US-09-883-825-6

Query Match 59.5%; Score 1591.5; DB 10; Length 530;
Best Local Similarity 61.2%; Pred. No. 5.7e-146;
Matches 309; Conservative 91; Mismatches 90; Indels 9; Gaps 1;

QY 19 LRYMVKQLENGEINIEELKKNLEYTASLEAVYIDETROIILDTDELEQELRSADVSEVR 78
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QY 79 DWLASTTQOARAKGRRAEKKPRFSIVHVAQAGIFVERMFRRTYTSVGYTSTAVLNCL 138
Db 95 DWLASTTFRKMGMTKKKPEEKPRFSIVHVAQAGIFVERMYRKYTHMVGLAYPAAVITL 154
QY 139 KNLDLWCDFVSLNQAAADHALRTIVFELLRHNLISRFKIPVFLMSFLDALETGYGY 198
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QY 199 KNPYHNOIHAADVTTQVHCLGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFIQT 258
Db 215 KNPYHNLHAADVTTQVHCLGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNFIQT 274
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Db 275 RSDVAILYNDRSVLENHHISSVFLMDDMMNIFNLTKDEFELRALVIEMLATDMSC 334
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Db 335 HFQOIKNIRSLQOPEGIDRAKTMSLILHAADISHPAKSWKLYHRTWMLMEFFRQGD 394
QY 379 EAEGLPFPPLCDRTSTVLAQSQIGFDIFVEPTFSLTDSPEKIIILIEDSKTKTPS 438
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RESULT 5
; Sequence 49, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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QY	360	VHSRWTALMEFFRQGOKEAELGLPFPLOCDRTSTLVAQSQIGFIDFIVEPTFSVLTDV	419
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QY	420	AKSVQPLADEDSKKNQPSQWQPSLD-VEVGDP-----NPD	457
Db	301	TEKIVSPLIDETSQGTGGQ---RRSSLNLSISSDAKRSKGVKTSKSGSAPINNSVSD	357
QY	458	VVSFRSTWVKRIQENKQWKRAASGITNQMISIDELSPCEEAPPSPAE	506
Db	358	YKSFRTWTEVHVHNRERAKV-----PKEBKAKEAE	392
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US-09-883-825-23			
Sequence 23, Application US/09883825			
Patent No. US20020151024A1			
GENERAL INFORMATION:			
APPLICANT: Beavo, Joseph A.			
Bentley, Kelley			
Sonnenburg, William K.			
Charbonneau, Harry			
TITLE OF INVENTION: DNA Encoding Mammalian			
Phosphodiesterases			
NUMBER OF SEQUENCES: 58			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &			
Bicknell			
STREET: Two First National Plaza, 20 South Clark			
Street			
CITY: Chicago			
STATE: Illinois			
COUNTRY: USA			
ZIP: 60603			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent In Release #1.0, Version #1.25			
APPLICATION NUMBER: US/09/883,825			
FILING DATE: 18-Jun-2001			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 09/123,783			
FILING DATE: <Unknown>			
APPLICATION NUMBER: 08/297,494			
FILING DATE: <Unknown>			
APPLICATION NUMBER: US 07/688,356			
FILING DATE: 04-APR-1991			
ATTORNEY/AGENT INFORMATION:			
NAME: No. US20020151024A1and, Greta E.			
REGISTRATION NUMBER: 35,302			
REFERENCE/DOCKET NUMBER: 27866/30822			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (312) 346-5750			
TELEFAX: (312) 984-9740			
TELEX: 25-3856			
INFORMATION FOR SEQ ID NO: 23:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 137 amino acids			
TYPE: amino acid			
TOPOLOGY: linear			
MOLECULE TYPE: protein			
SEQUENCE DESCRIPTION: SEQ ID NO: 23:			
US-09-883-825-23			
Query Match 25.0%; Score 668; DB 10; Length 137;			
Best Local Similarity 93.4%; Pred. No. 4,9e-57;			
Matches 128; Conservative 4; Mismatches 5; Indels 0; Gaps 0;			
QY	242	IHDYHTGTTNSFHQTKSECAIVYNDRSVLENHHISSVFRMLQDDMNIFINLTDEFY	301







Db 334 -HADVAYHNNIHAADVQSTHLLSTPALEAVFTOLEILAAIFASAIHDVDHPGVSNQFL 392  
QY 256 IOTKSECAIVYNDRSVLENNHSSVFRMLQDDMMIFNLTKDEFVELRALVIEVMTATD 315  
Db 393 INTNSELALMYNDSSVLENNHHLAVGFKLLQEECDIFQNLTKKQSRKMYIDIVLATD 452  
QY 316 MSCHPQOVKTKMTALQOLE-----RIDKPKALSLLHAADISHPTKQWLVSRSW 364  
Db 453 MSKHNLLADLKTWVETKVTSSGVLILLDNDYSDRIQVLMVHCADLSNPTKPLQLYRQW 512  
QY 365 TKALMEEFROGDKAEGLCLPESPLCDRTSTLVAQSOIGFIDFIVEPTFSVLTDAEKS 424  
Db 513 TDRIMEEFROGDRERERMEISPMCDKHNASVEKSVQGVFIDYIVHPLMETWADLVHPDA 572  
QY 425 QPLAD--EDSKSKNPQSFQWRQPSLDVEVDGPNPDVVSFRSTWVKRIQENKOKWKERAAS 482  
Db 573 QDILTLEDNR-----EWQSTIP-QSPSPAPD-----DPEEGROGQTEKFQF 614  
QY 483 GITNQMSIDELSPCEEAPPSPAD 507  
Db 615 ELT--LEEDGESDTEKDSGSQVEED 637

RESULT 15  
US-10-076-597-50  
; Sequence 50, Application US/10076597  
; Publication No. US20030045490A1  
; GENERAL INFORMATION:  
; APPLICANT: Dale, Roderic M. K.  
; APPLICANT: Arrow, Amy  
; APPLICANT: Thompson, Terry  
; TITLE OF INVENTION: Antisense Phosphodiesterase Inhibitors  
; FILE REFERENCE: OLIG-003CIP  
; CURRENT APPLICATION NUMBER: US/10/076,597  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/364,626  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/223,586  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 50  
; LENGTH: 745  
; TYPE: PRT  
; ORGANISM: human  
US-10-076-597-50

Query Match 23.1%; Score 617.5; DB 15; Length 745;  
Best Local Similarity 29.9%; Pred. No. 5.6e-51;  
Matches 151; Conservative 105; Mismatches 174; Indels 75; Gaps 14;  
QY 24 KOLENGEI-NIEELKKNLEYTASLEAVYIDETQILDEQLERDAVPSEVRDMLA 82  
Db 245 KRLNRELTHLSEMSRSGNQVSEFISNTFLDKQHEV-----EIPSP----- 285  
QY 83 STFTQARAKGR-AFEKPKRSIVHVAQAGIFVERMERFRTYTSVGPYST-----AVL 135  
Db 286 ----TQKEKKRPSQSGVKKLMHSSSL-----TNSSI-PREGVKTQEDVLA 331  
QY 136 NCLKNLDLWCFVFSINQAADHALRTIVFELLTRHNLISREKIPVFLMSFALDEYGY 195  
Db 332 KELEDVKNKGLHVFRIAELSGNRPLTVIMHTIFQERDLKTKPIVDILITVMTLEDHY 391  
QY 196 GYKKNPNQIHAADVOTVCHVFLRTGMVHCLSEIELLAIIFAAAIHDHYEHTGTNSPH 255  
Db 392 -HADVAYHNNIHAADVQSTHLLSTPALEAVFTOLEILAAIFASAIHDVDHPGVSNQFL 450  
QY 256 IOTKSECAIVYNDRSVLENNHSSVFRMLQDDMMIFNLTKDEFVELRALVIEVMTATD 315  
Db 451 INTNSELALMYNDSSVLENNHHLAVGFKLLQEECDIFQNLTKKQSRKMYIDIVLATD 510  
QY 316 MSCHPQOVKTKMTALQOLE-----RIDKPKALSLLHAADISHPTKQWLVSRSW 364

Db 511 MSKHNLLADLKTWVETKVTSSGVLILLDNDYSDRIQVLMVHCADLSNPTKPLQLYRQW 570  
QY 365 TKALMEEFROGDKAEGLCLPESPLCDRTSTLVAQSOIGFIDFIVEPTFSVLTDAEKS 424  
Db 571 TDRIMEEFROGDRERERMEISPMCDKHNASVEKSVQGVFIDYIVHPLMETWADLVHPDA 630  
QY 425 QPLAD--EDSKSKNPQSFQWRQPSLDVEVDGPNPDVVSFRSTWVKRIQENKOKWKERAAS 482  
Db 631 QDILTLEDNR-----EWQSTIP-QSPSPAPD-----DPEEGROGQTEKFQF 672  
QY 483 GITNQMSIDELSPCEEAPPSPAD 507  
Db 673 ELT--LEEDGESDTEKDSGSQVEED 695

Search completed: August 11, 2003, 01:25:35  
Job time : 339 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2003, 00:55:06 ; Search time 44 seconds  
(without alignments)  
1127.796 Million cell updates/sec

Title: US-09-663-481-1

Perfect score: 2676

Sequence: 1 MANPVPVQSHLQPIRLR.....EEAPPSPAEDHNGNGLD 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2582	96.5	536	1 JC6129	3',5'-cyclic-nucle
2	2491	93.1	535	1 A44161	3',5'-cyclic-nucle
3	2489	93.0	535	1 A46378	3',5'-cyclic-nucle
4	2484.5	92.8	534	1 A44162	3',5'-cyclic-nucle
5	1610.5	60.2	519	2 T14783	3',5'-cyclic-nucle
6	1594	59.6	768	2 T10796	hypothetical prote
7	1591.5	59.5	530	1 A45334	3',5'-cyclic-nucle
8	1503	56.2	491	2 A40283	3',5'-cyclic-nucle
9	1254.5	46.9	664	2 T24459	hypothetical prote
10	638	23.8	549	2 T16769	hypothetical prote
11	626	23.4	712	2 S71626	3',5'-cyclic-nucle
12	622.5	23.3	844	2 I53865	phosphodiesterase
13	620	23.2	610	2 I67946	3',5'-cyclic-nucle
14	617.5	23.1	584	2 B53109	3',5'-cyclic-nucle
15	617.5	23.1	673	2 I61358	3',5'-cyclic-nucle
16	616	23.0	536	2 I67945	3',5'-cyclic-nucle
17	615	23.0	562	2 I59143	cAMP phosphodiesterase
18	613	22.9	786	2 I61354	phosphodiesterase
19	613	22.9	836	2 A54442	3',5'-cyclic-nucle
20	612.5	22.9	672	2 I61259	3',5'-cyclic-nucle
21	611	22.8	777	2 S65543	3',5'-cyclic-nucle
22	610.5	22.8	564	2 J61519	3',5'-cyclic-nucle
23	609.5	22.8	564	2 A40949	cyclic-AMP phospho
24	542	20.3	323	2 S53448	3',5'-cyclic-nucle
25	516	19.3	267	2 B33904	cAMP phosphodiesterase
26	511	19.1	1054	2 T30901	cyclic nucleotide
27	481.5	18.0	1112	2 S70522	cyclic nucleotide
28	481.5	18.0	1141	2 A44093	cGMP-inhibited cAM
29	478.5	17.9	1108	2 A48508	cyclic-nucleotide

RESULT 1

JC6129

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63k  
N:Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1  
C:Species: Homo sapiens (man)  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 21-Jul-2000  
C:Accession: JC6129; G02260  
R:Jiang, X.; Li, J.; Faskind, M.; Epstein, P.M.  
Proc. Natl. Acad. Sci. U.S.A. 93: 11236-11241, 1996  
X:Title: Inhibition of calmodulin-dependent phosphodiesterase induces apoptosis in hu  
A:Reference number: JC6129; MUID:97008163; PMID:8855339  
A:Accession: JC6129  
A:Molecule type: mRNA  
A:Residues: 1-536 <JIA>  
A:Cross-references: GB:U56976; NID:gl621591; PIDN:AAC50769.1; PID:gl621592  
A:Experimental source: lymphoblastoid B-cell  
R:Houslay, M.D.; Erdogan, S.; Rena, G.; Sullivan, M.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: H00937  
A:Accession: G02260  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 201-203, 'W', 205-358, 'S', 360-384 <HOU>  
A:Cross-references: EMBL:U40584; NID:gl110534; PID:gl110535  
C:Comment: This enzyme is a useful target for inducing the death of leukemic cells.  
C:Genetics:  
A:Gene: GDB:PDE1B; PDESLB  
A:Cross-references: GDB:I20264; OMIM:171891  
A:Map position: 16p13.11  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3'  
C:Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric dieste  
F:222-439/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 96.5%; Score 2582; DB 1; Length 536;  
Best Local Similarity 100.0%; Pred. No. 3.3e-184;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	19	LYRMVQLENGEINTEELKKNLEYTASLEAVYIDETQILDTDEQLRLSDAVPSEVR	78
DB	39	LYRMVQLENGEINTEELKKNLEYTASLEAVYIDETQILDTDEQLRLSDAVPSEVR	98
QY	79	DWLASTFTQQAARAKERRAEKPKFRSIVHVAOAGFVFERMFRRTVTSVGPYSTAVLNCL	138
DB	99	DWLASTFTQQAARAKERRAEKPKFRSIVHVAOAGFVFERMFRRTVTSVGPYSTAVLNCL	158
QY	139	KNLDLWCDFVSLNQAADHDLRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKY	198
DB	159	KNLDLWCDFVSLNQAADHDLRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKY	218
QY	199	KPNYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYHTGTNSFHQT	258
DB	219	KPNYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYHTGTNSFHQT	278



```

|||||
398 EAELGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSLVTDVAEKSVQPLADDDSKPSQP 457
|||||
QY 439 SFQWRQPSLDVVEGPNPDVVSFRSTWVKRIQENKQKWKRAASGITNOMSIDELSPCEE 498
|||||
Db 458 SFQWRQPSLDVVEGPNPDVVSFRSTWVKRIQENKQKWKRAASGITNOMSIDELSPCEE 517
|||||
QY 499 EAPSPSPAEDEHNQNGNLD 516
|||||
Db 518 EAPSSPAEDEHNQNGNLD 535
|||||

RESULT 4
A44162
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp
N:Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Nov-1999
C:Accession: A44162; B40283
R: Bentley, J.K.; Kadlecik, A.; Sherbert, C.H.; Seger, D.; Sonnenburg, W.K.; Charbonneau,
J. Biol. Chem. 267, 18676-18682, 1992
A: Title: Molecular cloning of cDNA encoding a "63"-kDa calmodulin-stimulated phosphodies
A: Reference number: A44162; MUID: 92406781; PMID: 1326531
A: Accession: A44162
A: Molecule type: mRNA
A: Residues: 1-534 <BEN>
A: Cross-references: GB:M94867; NID: g162782; PIDN: AAA74558.1; PID: g162783
A: Experimental source: brain
A: Note: sequence extracted from NCBI backbone (NCBIP: l13352)
R: Novack, J.P.; Charbonneau, H.; Bentley, J.K.; Walsh, K.A.; Beavo, J.A.
Biochemistry 30, 7940-7947, 1991
A: Title: Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent cyclic nuc
A: Reference number: A40283; MUID: 91329366; PMID: 1651112
A: Accession: B40283
A: Molecule type: protein
A: Residues: 29-45, 'IP', 48, 'R', 50-52, 'IS', 55-85, 196-215, 277, 'D', 279, 'T', 281-287, 'T', 289-2
A: Experimental source: brain
C: Comment: This enzyme is a useful target for inducing the death of leukemic cells, and
C: Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C: Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h
F: 220-437/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 92.8%; Score 2484.5; DB 1; Length 534;
Best Local Similarity 96.0%; Pred. No. 5.9e-177;
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 19 LRYMKQLENGEINTEELKKNLEYTASLLEAVYIDETRIILDETELQELRSDAVPSEVR 78
|||||
Db 38 LRYMKQLENGEINTEELKKNLEYTASLLEAVYIDETRIILDETELQELRSDAVPSEVR 97
|||||

QY 79 DWLASTFTQARAKGRRAEKEPKFRSIVHVAQVGFVERMFRRTVTSVGPYTSVAVLNCL 138
|||||
Db 98 DWLASTFTQOTRAG-PSEKEPKFRSIVHVAQVGFVERMFRRTVTSVGPYTSVAVLNCL 156
|||||

QY 139 KNLDLWCFDVSINQAADHALRTIVFELLTHNLISRKIPTVFLMSFLDALETGYGKY 198
|||||
Db 157 KNVDLWCFDVSINRAADHALRTIVFELLTHNLISRKIPTVFLMTFLDALETGYGKY 216
|||||

QY 199 KNPYHNOHAADVTQVHCFLRTGMVHCLSEIELLAIFAAIHDIYHGTGNTSFHIQT 258
|||||
Db 217 KNPYHNOHAADVTQVHCFLRTGMVHCLSEIELLAIFAAIHDIYHGTGNTSFHIQT 276
|||||

QY 259 KSECAIVNDRSVLENHHISSVFLRMQDDEMNIFNLTKDEFELRALVEMVLATDMSC 318
|||||
Db 277 KSECALLYNDRSVLENHHISSVFLRMQDDEMNIFNLTKDEFELRALVEMVLATDMSC 336
|||||

QY 319 HFQVQTKMTALQQLERIDKPKALSLLHAADISHPTKQWLHSHRWTKALMEEFPRQGD 378
|||||
Db 337 HFQVQKMKTAQLQELRIDKPKALSLLHAADISHPTKQWLHSHRWTKALMEEFPRQGD 396
|||||

QY 379 EAELGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSLVTDVAEKSVQPLADEDSKSNQP 438
|||||
Db 397 EAELGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSLVTDVAEKSVQPTGDDDSKSNQP 456
|||||

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QY 439 SFQWRQPSLDVVEGPNPDVVSFRSTWVKRIQENKQKWKRAASGITNOMSIDELSPCEE 498
|||||
Db 457 SFQWRQPSLDVVEGPNPDVVSFRSTWVKRIQENKQKWKRAASGITNOMSIDELSPCEE 516
|||||
QY 499 EAPSPSPAEDEHNQNGNLD 516
|||||
Db 517 EAPASPAEDEHNQNGNLD 534
|||||

RESULT 5
T14783
hypothetical protein DKFZp586G0221.1 - human
C: Species: Homo sapiens (man)
C: Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C: Accession: T14783
R: Ottenwälder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A: Reference number: Z18184
A: Accession: T14783
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-519 <OTT>
A: Cross-references: EMBL: AL110263
A: Experimental source: adult uterus; clone DKFZp586G0221
C: Genetics:
A: Note: DKFZp586G0221.1
C: Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3'
F: 202-419/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 60.2%; Score 1610.5; DB 2; Length 519;
Best Local Similarity 60.9%; Pred. No. 5.9e-112;
Matches 307; Conservative 87; Mismatches 87; Indels 23; Gaps 2;

```

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QY 1 MANVPVQRSHLQGPILRLRYVMVKQLENGEINTEELKKNLEYTASLLEAVYIDETRIIL 60
|||||
Db 1 MDDHVTIRKKHLQRPILRLCLVKQLERGDVNVVDLKKNIYAAASVLEAVYIDETRIIL 60
|||||

QY 61 TEDELQELRSDAVPSEVRDMLASTFTQARAKGRRAEKEPKFRSIVHVAQVGFVERMFR 120
|||||
Db 61 TEDELSIDITDVSVPSEVRDMLASTFTIRKMGMTKKKPEEKPKFRSIVHVAQVGFVERMFR 120
|||||

QY 121 RYTSVGPYTSVAVLNCLNLDLWCFDVSINQAADHALRTIVFELLTHNLISRKIPT 180
|||||
Db 121 KTYHVMGLAYPAAVITLKDVKDVSDFEALNEASGEHSLKPMIYELTRYDLINRFKIP 180
|||||

QY 181 TVFLMSFLDALETGYGKYKNPYHNOHAADVTQVHCFLRTGMVHCLSEIELLAIFAA 240
|||||
Db 181 VSLTITFAEALVEGVSKYKNPYHNLHHAADVTQVHYIMLHTGIMHMLTELEILAMVFAA 240
|||||

QY 241 AHDYEHTGTTNSFHIOTKSECAIVNDRSVLENHHISSVFLRMQDDEMNIFNLTKDEF 300
|||||
Db 241 AHDYEHTGTTNHFHIOTRSDVAILYNDRSVLENHHVSAAYRLMQEEMNILLNSKDDW 300
|||||

QY 301 VELRALVEMVLATDMSCHFQVQTKMTALQQLERIDKPKALSLLHAADISHPTKQWL 360
|||||
Db 301 RDLRLNVLVEMVLSTDMSGHFQVQTKMTALQQLERIDKPKALSLLHAADISHPAKSWKL 360
|||||

QY 361 HSRWTKALMEEFPRQGDKEAELGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSLVTDVA 420
|||||
Db 361 HYRWTKALMEEFPRQGDKEAELGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSLTDT 420
|||||

QY 421 EKSVQPLADEDSKSNQPSFQWRQPSL-----DVEVGDPNP-----D 457
|||||
Db 421 EKVIPLIEASKAETSSVVSASSSTTVIGLHTADALRRNRTKGSMSDGSYSPTYSLAAV 480
|||||

QY 458 VVSFRSTWVKRIQENKQKWKRAA 481
|||||
Db 481 LKSFKNLVDIIQONKRWKELAA 504
|||||

```

RESULT 6  
T10796



QY 490 IDELSPEEE 499  
Db 515 NSDLVNAEEK 524

RESULT 8  
A40283  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), calmodulin-dependent, 59K card  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jan-2000  
C:Accession: A40283  
R:Novack, J.P.; Charbonneau, H.; Bentley, J.K.; Walsh, K.A.; Beavo, J.A.  
Biochemistry 30, 7940-7947, 1991  
A:Title: Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent cyclic nu  
A:Reference number: A40283; MUID:91329366; PMID:1651112  
A:Accession: A40283  
A:Molecule type: protein  
A:Residues: 1-491 <NOV>  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
C:Keywords: calmodulin binding; cardiac muscle; heart; phosphoric diester hydrolase  
F:196-396/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NP>

Query Match 56.2%; Score 1503; DB 2; Length 491;  
Best Local Similarity 57.9%; Pred. No. 5.4e-104;  
Matches 294; Conservative 90; Mismatches 92; Indels 32; Gaps 6;

QY 1 MANPVVORSHLGGPILRLRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETRIQILD 60  
Db 1 MODHTIRKHQRIPIRLURCLVQLEKGDVNWIDLKNIEYAASVLEAVYIDETRIQLD 60

QY 61 TEDELQELSDAVPSEVRDMLASTTQQARAKGRRAEKPFRSIVHVAQAGIFVERMFR 120  
Db 61 TDELSDIQSDVPSEVRDMLASTFMK-----KKSEKPRERSIVHVVQAGIFVERMYR 115

QY 121 RYTSVGPYTSYAVLNCNLKLDWCFVPSLNOAADHRLRTIVPELTLRNLISRFKIP 180  
Db 116 KSYHVMGLAYPEAVITLKDVKDFVFNALNEASGEHSLK-MIYELETRYDLINRFKIP 174

QY 181 TVFLMSFLDALGTGKYKNPYHNOIHAADVTQTVHCFLLRTGMVHCISEIELLAIIPAA 240  
Db 175 VSLCLAFPAEALVGVSKNPNYHNIHAADVTQTVHYIMLTGIMHWLFEILEILAVFPA 234

QY 241 AIHDEHTGTTNSFHIOKSECAIYVNDRSVLNHHISSVFRIMQDDENINILTKDF 300  
Db 235 AIHDEHTGTTNFIHQTRSDVAILYNDRSVLNHHVSAAYR-----MNVLINLSKDDW 288

QY 301 VELRALVIVMLATDMSCHFQOVKMTALQOLERIDPKALSLLHAAIDISHPTKQWLV 360  
Db 289 RDLRLNVLVIEL-----STKNIRNSLQOPEGLDK-KTMSLILHAAIDISHPAKSWKL 337

QY 361 HSRWTKALMEEFPROGDKAEGLPFLPCDRSTLTVAQSQIGFIDFIVEPTFSVLTDA 420  
Db 338 HIRWTMALMEEFLOGDKAEGLPFLPCDRKSTVAQSQIGFIDFIVEPTFSVLTST 397

QY 421 EKSVOPLADEDSKSNQPSFQWRQPSLDVEVD-----PNPDVVSFRSTWTKRQIE 471  
Db 398 EKIIILIEEDSKTTPSYGASRSRMKGTNDGYSPDYSLASVDLAKSFKNLSVDIIQQ 457

QY 472 NKQWKERASAGITNQMSIDELSPCEE 499  
Db 458 NKERWELAAQGEPPDHKNSDLVNAEEK 485

RESULT 9  
T24459  
hypothetical protein T04D3.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000  
C:Accession: T24459  
R:Kershaw, J.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: 219893

A:Accession: T24459  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-664 <WIL>  
A:Cross-references: EMBL:281114; PIDN:CAB03289.1; GSPDB:GN00019; CESP:T04D3.3  
A:Experimental source: clone T04D3  
C:Genetics:  
A:Gene: CESP:T04D3.3  
A:Map position: 1  
A:Introns: 52/3; 102/1; 152/2; 190/2; 355/3; 465/2; 553/3; 589/2; 634/1; 660/1  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology  
F:332-549/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NP>

Query Match 46.9%; Score 1254.5; DB 2; Length 664;  
Best Local Similarity 47.0%; Pred. No. 2.5e-85;  
Matches 255; Conservative 92; Mismatches 139; Indels 57; Gaps 11;

QY 8 QRSHLQGPIL----RLRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETRIQILD 63  
Db 138 KKSYNAPALESLEKLYILHQLNSQLPLEDLKRNIEYAALVLETAYNDETRICDEDD 197

QY 64 ELQELSDAVPSEVRDMLASTTQQARAKGRRAEKPFRSIVHVAQAGIFVERMFR 123  
Db 198 DIAEVTPTVPDEVRDLAATFTQNAAGKR---DKPKFSVANAIKRTGIFFEKLPRKQ 254

QY 124 TSVGPYTSYAVLNCNLKLDWCFVPSLNOAADHRLRTIVPELTLRNLISRFKIP 183  
Db 255 VVQCP-IPPEIAELMKEVCTNSFPQLNEVSEGHAKYVGFELFNRYGFMORFKVPLTA 313

QY 184 LMSFLDALGTGKYKNPYHNOIHAADVTQTVHCFLLRTGMVHCISEIELLAIIFAAAIH 243  
Db 314 LENYLSALEVGVSKNPNYHNVHAAADVTQSSHFMSLQSGTGLANSGLDELLAVLFGALIH 373

QY 244 DYEHGTGTTNSFHIOKSECAIYVNDRSVLNHHISSVFRIMQDDENINILTKDFVEL 303  
Db 374 DYEHGTGTTNFIHQTRSDVAILYNDRSVLNHHVSSCFRLMKEDDDKNIILTLTRDEYKEL 433

QY 304 RALVIVMLATDMSCHFQOVKMTALQOLERIDPKALSLLHAAIDISHPTKQWLVHSR 363  
Db 434 RNWVIEVLATDMSHFMOIKTKMSMLSLPEGLDKNKLCLIVHACDISHPAKPNLHER 493

QY 364 WTKALMEEFPROGDKAEGLPFLPCDRSTLTVAQSQIGFIDFIVEPTFSVLTDAEKS 423  
Db 494 WTEGVLEEFPROGDLKAEGLPFLPCDRHTVHVAQSGIFIDFIVEPTMVVCGELLVKM 553

QY 424 VQPL-----ADEDS-----KSNQPSFQWRQ-----SLDVE 450  
Db 554 VEPLVSLPPTDSLFPSPVDGDDKSPSNALSLPLDLRNSSTSPSSIRTRIPNLVAGKLDI- 612

QY 451 VGDPNPDVVSFRSTWVKRTOENKQKWKRAASGITNQMSIDELSPCEEAPPSPADEHN 510  
Db 613 ---PTP-----WMKFLHENKAHWKRAAKE-EERKIKEAA--EAEAAKQVE-ENK 657

QY 511 QNG 513  
Db 658 ENG 660

RESULT 10  
T16769  
hypothetical protein R153.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jun-2000  
C:Accession: T16769  
R:Kirsten, J.  
submitted to the EMBL Data Library, June 1995  
A:Description: The sequence of C. elegans cosmid R153.  
A:Reference number: Z18573  
A:Accession: T16769  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-549 <KIR>  
A:Cross-references: EMBL:U28729; NID:g861238; PID:g861239; PIDN:AAA68292.1; CESP:R153

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:R153.1

A;Introns: 25/2; 56/3; 91/1; 116/3; 163/3; 304/3; 338/1; 389/3; 430/3; 491/3

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'

F;281-509/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.8%; Score 638; DB 2; Length 549;

Best Local Similarity 32.8%; Pred. No. 1.4e-39;

Matches 150; Conservative 89; Mismatches 157; Indels 62; Gaps 12;

Qy 24 KOLENGEI-NIEELKKNLEYTASLEAVYIDETQRIIDTEDELQELSDAVPSVRDMLA 82

Db 118 KMLNKLSEFAESSKSTQSKFLITTYNDKEDEPSIEI-----VPIEV----- 164

Qy 83 STFTQARAKRAAEKPKERSIVHVAQAGIF-----VERMFRYTSVGTSTAVLNC 137

Db 165 ----QGSTSG-----PMTLSILKKAQTAAMNKISGVRLKRAPSHDGHVPEV-----VNC 211

Qy 138 -----LKNLDLWCFDPSLNQADDAHALRTIVFELLTRHNLISRKPIPTVFLMSFLDA 190

Db 212 ARETAVHQRDDGPDVKIDELSKNHSITVTFSLRQNLNFKTEIHOSHTLVTVLLN 271

Qy 191 LETGYGKYNPNQIHAADVTQVHCFLRTGMVHCLSEIELLAIIFAAAIHDEHTGT 250

Db 272 LEHHY--RNHYHNF IHAADVAQSMHVLMSPLVTEVTDLEVLAAIFAGAVHDVHPGF 329

Qy 251 TNSFHITKSECAIVYNDRSVLENHHISVFRMLQDDMNIFNLTKDEFVELRALVIEM 310

Db 330 TNOYLINSNELAIMYNDSEVLQHLAVAFKLLQDSNCDPLANLSRKQRLQPKIVIDM 389

Qy 311 VLATDMSCHFOQVTKMTALQO-----LERI-DKPKALSLLHAAADISHPKQWL 359

Db 390 VLATDMSKMSLLADLTKTVEAKVAGNNVILVDKYNKIQVLSQSMTHLADLSNPKPIE 449

Qy 360 VHSRWTKALMEFFRQDKAEGLPFLPCDRTSTLVAQSGIQTDFIVEPTFVSLTDV 419

Db 450 LYQOWNRIMEEYWRQDKKEGLLEISPMCDRGNTIEKSGVGFIDYIYHPLYETWADL 509

Qy 420 AEKSVQPLADESKSNQPSFQWRQPSLDVEGDPNPD 457

Db 510 VYPDAQNILDOLEENR-----EWVQSRPEE-----PD 537

RESULT 11

S71626

N;Alternate names: 3',5'-cyclic nucleotide phosphodiesterase (EC 3.1.4.17), CAMP-specific - human

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1997; #sequence\_revision 12-Dec-1997 #text\_change 17-Nov-2000

C;Accession: S71626; I61356

R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.

FEBs Lett. 359, 305-310, 1995

A;Title: Molecular cloning and functional expression in yeast of a human CAMP-specific P

A;Reference number: S71626; MUID:95145731; PMID:7843419

A;Accession: S71626

A;Molecule type: DNA

A;Residues: 1-712 <ENG>

A;Cross-references: EMBL:246632; NID:g727222; PIDN:CAA86601.1; PID:g727223

A;Experimental source: substantia nigra

R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,

Mol. Cell. Biol. 13, 6558-6571, 1993

A;Title: A family of human phosphodiesterases homologous to the dunce learning and mem

A;Reference number: A54442; MUID:94019330; PMID:8413254

A;Accession: I61356

A;Status: preliminary;

A;Molecule type: mRNA

A;Residues: 462-712 <RES>

A;Cross-references: GB:L20968; NID:g347125; PIDN:AAA03591.1; PID:g347126

C;Genetics:

A;Gene: HSPDB4C1

C;Function:

A;Description: CAMP hydrolysis; converts CAMP to non-cyclic AMP

A;Pathway: cyclic nucleotide metabolism

A;Note: expressed in various tissues but not in cells of the immune system

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent;

C;Keywords: phosphoric diester hydrolase

F;367-615/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.4%; Score 626; DB 2; Length 712;

Best Local Similarity 29.2%; Pred. No. 1.6e-38;

Matches 151; Conservative 108; Mismatches 205; Indels 54; Gaps 12;

Qy 7 VORSHLOGLILRLRYMVKOLENGEI-NIEELKKNLEYTASLEAVYIDETQRIIDTEDEL 65

Db 223 LQPHSHVGEAMSNKF--KRILNRELTHLSRSGNQVSEYISRTFLDQ-----QTEVEL 275

Qy 66 QELRSDAVPSEVRDMLASTTQOARAKRAAEKPKERSIVHVAQAGIFVERMPRRYTS 125

Db 276 PKVTAEEAPQPM-----SRISG-----LHGCHSASLSASATVPR-----G 311

Qy 126 VGYTSTAVLNCNLKNDLWCFDPSLNQADDAHALRTIVFELLTRHNLISRKPIPTVFLM 185

Db 312 VQDQEQALAKELEDTKNGLDVFKVADVSGNRPPLTAIIFSFQERDLLTFFQIPADTLA 371

Qy 186 SPLDALETGYGKYNPNQIHAADVTQVHCFLRTGMVHCLSEIELLAIIFAAAIHDEY 245

Db 372 TYLLMLE-GHYHANVAYHNSLHAADVAQSTHVLATPALEAVFTDLELAAALFASAIHDV 430

Qy 246 EHTGTTNSPHIOTKSECAIVYNDRSVLENHHISVFRMLQDDMNIFNLTKDEFVELRA 305

Db 431 DHPGVSNQOFLINTNSDALMYNDASVLENHHLAVGFKLQAEKNCDFQNLSSAKQRLSRR 490

Qy 306 LVTEMLVATDMSCHFQVTKMTALQOLE-----RIDKPKALSLLHAAADISHP 354

Db 491 MVIDMVLATDMSKHMNLADLTKMTVETKVTSLGVLLLDNYSRDIQVLQNLVHCADLSNP 550

Qy 355 TKQWLVSRTWKALMEFFRQDKAEGLPFLPCDRTSTLVAQSGIQTDFIVEPTFES 414

Db 551 TKPLPLRYQWTDRIAMAEFFQGDRESGLDISPMCDKHSTAEKVSQGVGIDYIAHPLWE 610

Qy 415 VLTDVAEKSVOPLAD--EDSKSNQPSFQWRQPSLDVEGDP---NPDVVYSFSTWVKRI 469

Db 611 TWADLVHPDAQDLDTLED---NREWYQSKIPRPSDLTNPRDGDPRDQFQFELTLEAE 666

Qy 470 OENKOKWKPRASAGITNO-NSIDELSPCEEEAPSPAE 506

Db 567 EDEDEEEGEETALAKEALELPTTELLSPFAGDPDGD 704

RESULT 12

I53865

Phosphodiesterase - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 02-Sep-2000

C;Accession: I53865

R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian c

A;Reference number: I53865; MUID:95047482; PMID:7958996

A;Accession: I53865

A;Status: preliminary;

A;Molecule type: mRNA

A;Residues: 1-844 <RES>

A;Cross-references: GB:L27057; NID:g3334904; PIDN:AAC27098.1; PID:g436004

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology

F;418-646/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.3%; Score 622.5; DB 2; Length 844;

Best Local Similarity 30.6%; Pred. No. 3.7e-38;

Matches 161; Conservative 99; Mismatches 185; Indels 85; Gaps 16;

Qy 4 PVPV-ORSHLOGP-----ILRLRYMVKOLEN-----GEINIEE 35

Db 197 PIPSNKRSLPGPPSYCKATLSEETCQQLARETLEELDWCLEQETMQYRSVSEMASHK 256



```

A:Accession: U38416
A:Molecule type: mRNA
A:Residues: 7C-507, /P, /509-673 <R2>
A:Cross-references: EMBL:U02882; NID:9433346; PIDN:AAC13745.1; PID:9433347
C:Genetics:
A:Gene: GDB:PCB4D; DPDE3
A:Cross-references: GDB:132541; OMIM:600129
A:Map position: 5q12-5q12
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent
C:Keywords: cAMP binding; phosphoric diester hydrolase
F:325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match      23.1%; Score 617.5; DB 2; Length 673;
Best Local Similarity 29.9%; Pred. No. 6.3e-38;
Matches 151; Conservative 105; Mismatches 174; Indels 75; Gaps

24 KOLENGEI-NTEELKKNLEYTASLEAVYIDETQRILDTDEQLERSDAVPSEVRDLWA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
173 KRMLNRELIHSEMSRSGNQVSEIINSTFLDKQHEV-----EIPSP-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

83 STFTQQAARAKRR-AEKKPRFSIVHAOVAQIGIVERMFRRTYTSVGPTYST-----AVL
214 ---TQKEKKKKRPMISOIGVKMLHSSSL-----TNSSI-PREGVKTEQEDVLWA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

136 NCLKNLDLWCDFVFLSNQAADHAIIRTVFELLTRHNLSRFXIPVFLMSFLDALETGY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
260 KELEDYNGKGLHFVRIAEALSGNRPILVIMHTIQRDLDTKFTPIVDYTLITVLMLEDRY
136 3KYNPYHNQIHAADVDTQTVHCFELRRITGMVHCLSEIELLAIIPAAIHODYEHTGTTNSFH
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
320 -HADYAYHNHHAADVQVSTHVLSTPALBAVFTDLEILAAIPASAIHVDVHPGVSNQFL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

256 IQTSECAIYVYNDRSVLNHHISSVFLMQDDMMNFIINLTKEFVELRALVIEWVLAD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
379 INTNSEALMYNDSVLENHHLAVGFKLLQEECDIFQNLTKKQROSLRKMWDIVLAD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
316 MSCHFQQVKTKMTALQOLE-----RIDKPALSLLHAAIDSHPTKQWLHVSRW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
439 MSKHNNLADLTKTWETKKVTSGLVLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

365 TKALMEEPFROGDKAEALGLPFSPLCDRTSLVAQSOIGFIDFIVETFTSVLTDAVEKSV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
499 TDRIMEEPFROGDRERGERGEIISPMCKDHNASVEKSOVGFDIVIHPLMETWADLVHPDA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

425 QPLAD--EDSKSNQKPSFQWRQPSLDVEVGDPNPVVYFSTRSTVWKVKIQENKQKWKRAAS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
559 QDILDLTLEDNR-----EWYQSTIP-QSPSPAPD-----DPEEGROGQTEKFOF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

483 GITNQMSIDELSPCEEAPPSPAPD 507
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
601 ILT--LEEDGESDTEKSGGSGVED 623
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: August 11, 2003, 01:12:42  
Job time : 46 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 10, 2003, 22:31:31 ; Search time 39 seconds  
(without alignments)  
622.199 Million cell updates/sec

Title: US-09-663-481-1  
Perfect score: 2676  
Sequence: 1 MANPVQVORHLQGFILRL.....EEAPPSPAEDHNONGNLD 516

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2582	96.5	536	1 CN1B_HUMAN	Q01064 homo sapien
2	2491	93.1	535	1 CN1B_RAT	Q01066 rattus norv
3	2489	93.0	535	1 CN1B_MOUSE	Q01065 mus musculu
4	2484.5	92.8	534	1 CN1B_BOVIN	Q01061 bos taurus
5	1595	59.6	654	1 CN1C_MOUSE	Q64338 mus musculu
6	1594	59.6	768	1 CN1C_RAT	Q63421 rattus norv
7	1593	59.5	709	1 CN1C_HUMAN	Q14123 homo sapien
8	1591.5	59.5	529	1 CN1A_BOVIN	P14100 bos taurus
9	1575	58.9	565	1 CN1A_MOUSE	Q61481 mus musculu
10	1568.5	58.6	534	1 CN1A_HUMAN	P54750 homo sapien
11	1254.5	46.9	664	1 YFGK_CAEEL	O18696 caenorhabdi
12	638	23.8	549	1 YST1_CAEEL	Q22000 caenorhabdi
13	637	23.8	844	1 CN1C_MOUSE	O89084 mus musculu
14	630	23.5	712	1 CN1C_HUMAN	Q08493 homo sapien
15	622.5	23.3	844	1 CN1A_RAT	P54748 rattus norv
16	618	23.1	886	1 CN1A_HUMAN	P27815 homo sapien
17	617.5	23.1	809	1 CN1D_HUMAN	Q08499 homo sapien
18	616	23.0	536	1 CN1C_RAT	P14644 rattus norv
19	615	23.0	721	1 CN1B_RAT	P14646 rattus norv
20	613	22.9	736	1 CN1B_HUMAN	Q07343 homo sapien
21	612.5	22.9	672	1 CN1D_RAT	P14270 rattus norv
22	611	22.8	777	1 CN1A_DROME	P12252 drosophila
23	505	18.9	793	1 REGA_DICDI	Q23917 dictyosteli
24	481.5	18.0	799	1 CN3B_MOUSE	Q61409 mus musculu
25	481.5	18.0	1112	1 CN3B_HUMAN	Q13370 homo sapien
26	481.5	18.0	1141	1 CN3A_HUMAN	Q14432 homo sapien
27	478.5	17.9	1108	1 CN3B_RAT	Q63085 rattus norv
28	470.5	17.6	1141	1 CN3A_RAT	Q62865 rattus norv
29	467	17.5	446	1 CN7B_MOUSE	Q9qxq1 mus musculu
30	464	17.3	456	1 CN7A_MOUSE	P70453 mus musculu
31	461.5	17.2	426	1 CN7A_RAT	O08593 rattus norv
32	457.5	17.1	482	1 CN7A_HUMAN	Q13946 homo sapien
33	449	16.8	450	1 CN7B_HUMAN	Q9np56 homo sapien

RESULT 1

ID	CN1B_HUMAN	STANDARD;	PRT;	536 AA.
AC	Q01064	Q92825;		
DE	01-APR-1993 (Rel. 25, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1B (EC 3.1.4.17) (Cam-PDE 1B) (63 kDa Cam-PDE).			
GN	PDE1B OR PDE1B1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97008163; PubMed=8855339;			
RA	Jiang X., Li J., Paskind M., Epstein P.M.;			
RT	"Inhibition of calmodulin-dependent phosphodiesterase induces apoptosis in human leukemic cells."			
RL	Proc. Natl. Acad. Sci. U.S.A. 93:11236-11241(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=98081132; PubMed=9419816;			
RA	Yu J., Frazier A.L.B., Wolda S.L., Florio V.A., Martins T.J., Snyder P.B., Harris E.A.S., McCaw K.N., Farrell C.A., Steiner B., Bentley J.K., Beavo J.A., Ferguson K., Gellinas R.;			
RT	"Identification and characterization of a human calmodulin-stimulated phosphodiesterase PDE1B1."			
RL	Cell. Signal. 9:519-529(1997).			
RN	[3]			
RP	SEQUENCE OF 222-337 FROM N.A.			
RX	MEDLINE=92406782; PubMed=1326532;			
RA	Repaske D.R., Swinnen J.V., Jin S.L.C., van Wyk J.J., Conti M.;			
RT	"A polymerase chain reaction strategy to identify and clone cyclic nucleotide phosphodiesterase cDNAs. Molecular cloning of the cDNA encoding the 63-kDa calmodulin-dependent phosphodiesterase."			
RL	J. Biol. Chem. 267:18683-18688(1992).			
CC	-!- FUNCTION: Has a preference for cGMP as a substrate.			
CC	-!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -> nucleoside 5'-phosphate.			
CC	-!- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF CALMODULIN IN THE PRESENCE OF CA(2+).			
CC	-!- SUBUNIT: Homodimer (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			

```

CC EMBL; U56976; AAC50769.1; -.
DR EMBL; U85078; AAC51872.1; -.
DR EMBL; M94539; AAA58405.1; -.
DR PIR; JC6129; JC6129.
DR PDB; 1LXR; 26-JUN-02.
DR Genew; HGNC:8775; PDE1B.
DR MIM; 171891; -.
DR GO; GO:0004117; F:calmodulin-dependent cyclic-nucleotide phos. . .; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR InterPro; IPR003607; Met_phosphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydroxylase; cAMP; cGMP; Calmodulin-binding; 3D-structure.
FT DOMAIN 127 47 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 197 496 CALMODULIN-BINDING (BY SIMILARITY).
FT CONFLICT 225 426 QI -> SM (IN REF. 2).
FT CONFLICT 337 337 S -> A (IN REF. 2).
SQ SEQUENCE 536 AA; 61379 MW; D15211AC32C756A4 CRC64;

Query Match          96.5%; Score 2582; DB 1; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.6e-179;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELRSDAVPSEVR 78
DB 39 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELRSDAVPSEVR 98
QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGTYSTAVLNCL 138
DB 99 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGTYSTAVLNCL 158
QY 139 KNLDLWCFDVSFNQADDDHALRTIVFELLTRNLISRKPIPTVFLMSFLDALETGYGKY 198
DB 159 KNLDLWCFDVSFNQADDDHALRTIVFELLTRNLISRKPIPTVFLMSFLDALETGYGKY 218
QY 199 KNPYHQIHAADVQTQVHCFLRTGMVHCLSEIELLAIIPAAAIHDYEHGTGTSNPHIQT 258
DB 219 KNPYHQIHAADVQTQVHCFLRTGMVHCLSEIELLAIIPAAAIHDYEHGTGTSNPHIQT 278
QY 259 KSCAIVYNDRSVLENHHISSVFRMLQDDENNIFNLTKDFVELRALVIEVLATDMSC 318
DB 279 KSCAIVYNDRSVLENHHISSVFRMLQDDENNIFNLTKDFVELRALVIEVLATDMSC 338
QY 319 HFQOVKTMKTALQQLERIDKPKALSLLHAADISHPTKQWLHSHRWTKALMEEFRRQGDK 378
DB 339 HFQOVKTMKTALQQLERIDKPKALSLLHAADISHPTKQWLHSHRWTKALMEEFRRQGDK 398
QY 379 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSVOPLADEDSKSNQP 438
DB 399 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSVOPLADEDSKSNQP 458
QY 439 SFQWRQPSLDVEYGDNDPVDVSRFTWVKRIQENKQWKERAASGITNOMSIDELSPCEE 498
DB 459 SFQWRQPSLDVEYGDNDPVDVSRFTWVKRIQENKQWKERAASGITNOMSIDELSPCEE 518
QY 499 EAPPSPAEDEHNGNGLD 516
DB 519 EAPPSPAEDEHNGNGLD 536

```

## RESULT 2

```

CNIB_RAT
ID CNIB_RAT STANDARD; PRT; 535 AA.
AC Q01066;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase
DE 1B (EC 3.1.4.17) (Cam-PDE 1B) (63 kDa Cam-PDE).
GN PDE1B OR PDE1B1.

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=52406782; PubMed=1326532;
RA Repaske L.R., Swinnen J.V., Jin S.L.C., van Wyk J.J., Conti M.;
RT "A polymerase chain reaction strategy to identify and clone cyclic
RT nucleotide phosphodiesterase cDNAs. Molecular cloning of the cDNA
RT encoding the 63-kDa calmodulin-dependent phosphodiesterase."
RL J. Biol. Chem. 267:18683-18688(1992).
CC "1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -
CC nucleoside 5'-phosphate.
CC "1- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF
CC CALMODULIN IN THE PRESENCE OF CA(2+).
CC "1- SUBUNIT: Homodimer.
CC "1- SUBCELLULAR LOCATION: Cytoplasmic.
CC "1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC
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CC
CC EMBL; M94537; AAA16530.1; -.
DR PIR; A44161; A44161.
DR InterPro; IPR003607; Met_phosphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydroxylase; cAMP; cGMP; Calmodulin-binding.
FT DOMAIN 127 47 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 196 495 CATALYTIC (BY SIMILARITY).
FT SEQUENCE 535 AA; 62259 MW; F98FFFE61F848F89 CRC64;

Query Match          93.1%; Score 2491; DB 1; Length 535;
Best Local Similarity 95.8%; Pred. No. 6.3e-173;
Matches 477; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 19 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELRSDAVPSEVR 78
DB 38 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELRSDAVPSEVR 97
QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGTYSTAVLNCL 138
DB 98 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGTYSTAVLNCL 157
QY 139 KNLDLWCFDVSFNQADDDHALRTIVFELLTRNLISRKPIPTVFLMSFLDALETGYGKY 198
DB 158 KNLDLWCFDVSFNQADDDHALRTIVFELLTRNLISRKPIPTVFLMSFLDALETGYGKY 217
QY 199 KNPYHQIHAADVQTQVHCFLRTGMVHCLSEIELLAIIPAAAIHDYEHGTGTSNPHIQT 258
DB 218 KNPYHQIHAADVQTQVHCFLRTGMVHCLSEIELLAIIPAAAIHDYEHGTGTSNPHIQT 277
QY 259 KSCAIVYNDRSVLENHHISSVFRMLQDDENNIFNLTKDFVELRALVIEVLATDMSC 318
DB 278 KSCAIVYNDRSVLENHHISSVFRMLQDDENNIFNLTKDFVELRALVIEVLATDMSC 337
QY 319 HFQOVKTMKTALQQLERIDKPKALSLLHAADISHPTKQWLHSHRWTKALMEEFRRQGDK 378
DB 338 HFQOVKTMKTALQQLERIDKPKALSLLHAADISHPTKQWLHSHRWTKALMEEFRRQGDK 397
QY 379 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSVOPLADEDSKSNQP 438
DB 398 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSVOPLADEDSKSNQP 457

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QY 439 SFQWRQPSLDVGDNDPVDVFRSTWVKRIQENKQKWKERAASGITNQMSIDELSPCEE 498  
Db 458 SFQWRQPSLDVGDNDPVDVFRSTWVKRIQENKQKWKERAASGITNQMSIDELSPCEE 517  
QY 499 EAPSPSPAEDHNONGNLD 516  
Db 518 EAPSPSPAEDHNONGNLD 535

## RESULT 3

CNIB\_MOUSE STANDARD; PRT; 535 AA.  
AC Q01085; O33384;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase  
DE 1B (EC 3.1.4.17) (Cam-PDE 1B) (63 kDa Cam-PDE).  
GN PDE1B OR PDE1B1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93066388; PubMed=1332068;  
RA Polli J.W., Kincaid R.L.;  
RT "Molecular cloning of DNA encoding a calmodulin-dependent  
RT phosphodiesterase enriched in striatum."  
RL Proc. Natl. Acad. Sci. U.S.A. 89:11079-11083(1992).  
RN [2]  
RP SEQUENCE OF 38-535 FROM N.A.  
RC STRAIN=129/SVJ;  
RX MEDLINE=98325610; PubMed=9657856;  
RA Reed T.M., Browning J.E., Blough R.I., Vorhees C.V., Repaske D.R.;  
RT "Genomic structure and chromosome location of the murine PDE1B  
RT phosphodiesterase gene."  
RL Mamm. Genome 9:571-576(1998).  
RN [3]  
RP SEQUENCE OF 221-336 FROM N.A.  
RX MEDLINE=92406782; PubMed=1326532;  
RA Repaske D.R., Swinnen J.V., Jin S.L.C., van Wyk J.J., Conti M.;  
RT "A polymerase chain reaction strategy to identify and clone cyclic  
RT nucleotide phosphodiesterase cDNAs. Molecular cloning of the cDNA  
RT encoding the 63-kDa calmodulin-dependent phosphodiesterase."  
RL J. Biol. Chem. 267:18683-18688(1992).  
CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =  
CC nucleoside 5'-phosphate.  
CC -1- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF  
CC CALMODULIN IN THE PRESENCE OF CA(2+).  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
CC FAMILY.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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CC EMBL; L01695; AAA39902.1; -  
CC EMBL; AF023343; AAC96022.1; -  
CC EMBL; AF023340; AAC96022.1; JOINED.  
CC EMBL; AF023341; AAC96022.1; JOINED.  
CC EMBL; AF023342; AAC96022.1; JOINED.  
CC EMBL; M94538; AAA37367.1; -  
CC PIR; A46378; A46378.  
CC MGD; MGI:97523; Pde1b.  
CC InterPro; IPR003607; Met\_phosphohydro.  
CC InterPro; IPR002073; PDEase.

Pfam; PF00233; PDEase; 1.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDEASE\_I; 1.  
KW Hydrolase; CAMP; CGMP; Calmodulin-binding.  
FT DOMAIN 27 47 CALMODULIN-BINDING (POTENTIAL).  
FT DOMAIN 196 495 CATALYTIC (BY SIMILARITY).  
FT CONFLICT 38 38 L -> M (IN REF. 2).  
FT CONFLICT 224 224 Q -> R (IN REF. 3).  
SQ SEQUENCE 535 AA; 61225 MW; F87A585537C8D1CD CRC64;

Query Match 93.0%; Score 2489; DB 1; Length 535;  
Best Local Similarity 95.8%; Pred. No. 8.8e-173;  
Matches 477; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 19 LRYMKQLENGEINIEELKKNLEYTASLLEAVYIDETQILDTDEQLRLSDAVPSEYR 78  
Db 38 LRYMKQLENGEINIEELKKNLEYTASLLEAVYIDETQILDTDEQLRLSDAVPSEYR 97  
QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPSTAVLNCL 138  
Db 98 DWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPSTAVLNCL 157  
QY 139 KNDLWCFDFVSLNQAADHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKY 198  
Db 158 KNDLWCFDFVSLNQAADHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKY 217  
QY 199 KNPYHQIHAADVQTQVHCFLRTGMVHCLSEIETELAIIFAAAIHDEYHTGTTNSPHIQ 258  
Db 218 KNPYHQIHAADVQTQVHCFLRTGMVHCLSEIETELAIIFAAAIHDEYHTGTTNSPHIQ 277  
QY 259 KSECAIVYNDRSVLENNHISVFRMLQDDMMNIFINLTDEFEVLEALVEMVLYATDMSC 318  
Db 278 KSECAIVYNDRSVLENNHISVFRMLQDDMMNIFINLTDEFEVLEALVEMVLYATDMSC 337  
QY 319 HFQOVTKMTALQOOLERIDKPKALSLLHAADSHPTKQWLVHSRWTKALMEEFRRQGD 378  
Db 338 HFQOVTKMTALQOOLERIDKPKALSLLHAADSHPTKQWLVHSRWTKALMEEFRRQGD 397  
QY 379 EAEGLPFPPLCDRTSTLVAQSIGFIDFIVEPTFSVLTDVAEKSVQPLADESKSNOP 438  
Db 398 EAEGLPFPPLCDRTSTLVAQSIGFIDFIVEPTFSVLTDVAEKSVQPLADESKSNOP 457  
QY 439 SFQWRQPSLDVGDNDPVDVFRSTWVKRIQENKQKWKERAASGITNQMSIDELSPCEE 498  
Db 458 SFQWRQPSLDVGDNDPVDVFRSTWVKRIQENKQKWKERAASGITNQMSIDELSPCEE 517  
QY 499 EAPSPSPAEDHNONGNLD 516  
Db 518 EAPSPSPAEDHNONGNLD 535

## RESULT 4

CNIB\_BOVIN STANDARD; PRT; 534 AA.  
AC Q01061;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase  
DE 1B (EC 3.1.4.17) (Cam-PDE 1B) (63 kDa Cam-PDE).  
GN PDE1B OR PDE1B1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Brain;  
RA MEDLINE=92406781; PubMed=1326531;  
RA Bentley J.K., Kadlec A., Sherbert C.H., Seger D., Sonnenburg W.K.,  
RA Charbonneau H., Novack J.P., Beavo J.A.;  
RT "Molecular cloning of cDNA encoding a '63'-kDa calmodulin-stimulated

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phosphodiesterase from bovine brain.";
J. Biol. Chem. 267:18676-18682(1992).
[2]
PARTIAL SEQUENCE.
TXSDP=Brain;
MEDLINE=91329366; PubMed=1651112;
Novack J.P., Charbonneau H., Bentley J.K., Walsh K.A., Beavo J.A.;
"Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent
cyclic nucleotide phosphodiesterases.";
Biochemistry 30:7940-7947(1991).
-1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =
nucleoside 5'-phosphate.
-1- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF
CALMODULIN IN THE PRESENCE OF CA(2+). REGULATED BY PHOSPHORYLATION
BY CAM-DEPENDENT PROTEIN KINASE II.
-1- SUBUNIT: Homodimer.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- TISSUE SPECIFICITY: EXPRESSED IN CENTRAL NERVOUS SYSTEM REGIONS.
MOST ABUNDANT IN BASAL GANGLIA. ALSO FOUND IN KIDNEY PAPILLA
AND ADRENAL MEDULA.
-1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY.
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EMBL; M94867; AAA74558.1; -.
PIR; A4162;
InterPro; IPR003607; Met_phosphohydro.
InterPro; IPR002073; PDEase.
Pfam; PF00233; PDEase.1.
PRINTS; PR00387; PD1ESTERASE1.
SMART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; CAMP; CGMP; Phosphorylation; Calmodulin-binding.
DOMAIN 27 47 CALMODULIN-BINDING (POTENTIAL).
DOMAIN 195 494 CATALYTIC (BY SIMILARITY).
SEQUENCE 534 AA; C86C3F48E0AE9B69 CRC64;
Query Match 92.88; Score 2484.5; DB 1; Length 534;
Best Local Similarity 96.08; Pred No 1.9e-172;
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
19 LRYMKQLENGEINIEELKNLEYTASLLEAVYIDETQRLDTEDEQLERSDAVPSEVR 78
||||| 19 LRYMKQLENGEINIEELKNLEYTASLLEAVYIDETQRLDTEDEQLERSDAVPSEVR 78
38 LRYMKQLENGEINIEELKNLEYTASLLEAVYIDETQRLDTEDEQLERSDAVPSEVR 97
||||| 38 LRYMKQLENGEINIEELKNLEYTASLLEAVYIDETQRLDTEDEQLERSDAVPSEVR 97
79 DWLASTTQQAARAKGRRAEKKPRISIVHQAQIFVERMFRRTYTSVGPTYSTAVLNCL 138
||||| 79 DWLASTTQQAARAKGRRAEKKPRISIVHQAQIFVERMFRRTYTSVGPTYSTAVLNCL 138
98 DWLASTTQQAARAKGRRAEKKPRISIVHQAQIFVERMFRRTYTSVGPTYSTAVLNCL 156
||||| 98 DWLASTTQQAARAKGRRAEKKPRISIVHQAQIFVERMFRRTYTSVGPTYSTAVLNCL 156
139 KNLDMCFDVFSLNQADHALRTIVFELLTRNLISREKIPVFLMSFLDALETGYGKY 198
||||| 139 KNLDMCFDVFSLNQADHALRTIVFELLTRNLISREKIPVFLMSFLDALETGYGKY 198
157 KNYDLMCFDVFSLNRAADHALRTIVFELLTRNLISREKIPVFLMFLDALETGYGKY 216
||||| 157 KNYDLMCFDVFSLNRAADHALRTIVFELLTRNLISREKIPVFLMFLDALETGYGKY 216
199 KNPYHNGIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDEYHGTGTTNSPHIQT 258
||||| 199 KNPYHNGIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDEYHGTGTTNSPHIQT 258
217 KNPYHNGIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDEYHGTGTTNSPHIQT 276
||||| 217 KNPYHNGIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDEYHGTGTTNSPHIQT 276
259 KSECAIYNDRSLENHHISSVFLRMDDMMNIFINLTDEKDFELRALVIEMLATDMSC 318
||||| 259 KSECAIYNDRSLENHHISSVFLRMDDMMNIFINLTDEKDFELRALVIEMLATDMSC 318
277 KSECAIYNDRSLENHHISSVFLRMDDMMNIFINLTDEKDFELRALVIEMLATDMSC 336
||||| 277 KSECAIYNDRSLENHHISSVFLRMDDMMNIFINLTDEKDFELRALVIEMLATDMSC 336
319 HFOQVKMTALQOOLERIDPKALSLLHAADISHTPKWLVHSRWTKALMEFFRQGD 378
||||| 319 HFOQVKMTALQOOLERIDPKALSLLHAADISHTPKWLVHSRWTKALMEFFRQGD 378
337 HFOQVKMTALQOOLERIDPKALSLLHAADISHTPKWLVHSRWTKALMEFFRQGD 396
||||| 337 HFOQVKMTALQOOLERIDPKALSLLHAADISHTPKWLVHSRWTKALMEFFRQGD 396
379 EAEGLPFPCLCDRTSTLVAQSQIGFDIFVEPFSVLTDVAEKSVQPTGDDSKSNQP 438
||||| 379 EAEGLPFPCLCDRTSTLVAQSQIGFDIFVEPFSVLTDVAEKSVQPTGDDSKSNQP 438

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RT PDE1A1 and PDE1A2 calmodulin-stimulated cyclic nucleotide  
phosphodiesterases.\*;  
J. Biol. Chem. 270:30989-31000(1995).  
[4]  
RN SEQUENCE OF 193-426.  
RC TISSUE=Brain;  
RX MEDLINE=87092242; PubMed=3025833;  
RA Charbonneau H., Beier N., Walsh K.A., Beavo J.A.;  
RT "Identification of a conserved domain among cyclic nucleotide  
phosphodiesterases from diverse species.\*";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:9308-9312(1986).  
CC -!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -  
nucleoside 5'-phosphate.  
CC -!- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF  
CALMODULIN IN THE PRESENCE OF CA(2+).  
CC -!- SUBUNIT: Homodimer.  
CC -!- ALTERNATIVE PRODUCTS:  
Event-Alternative splicing; Named isoforms-2;  
Name=2; Synonyms=PDE1A2;  
IsoId=PI4100-1; Sequence=Displayed;  
Name=1; Synonyms=PDE1A1;  
IsoId=PI4100-2; Sequence=VSP\_004546;  
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
FAMILY.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; M90358; AAA74560.1; -;  
DR EMBL; L34069; AAA92555.1; -;  
DR PIR; A45334; A45334.  
DR InterPro; IPR003607; Met\_phosphohydro.  
DR InterPro; IPR002073; PDEase.  
DR Pfam; PF00233; PDEase; 1.  
DR SMART; SM00471; Hdc; 1.  
DR PROSITE; PS00126; PDEASE\_I; 1.  
KW Hydrolase; cAMP; cGMP; Multigene family; Alternative splicing;  
KW Calmodulin-binding.  
FT INIT\_MET 0 0  
FT DOMAIN 23 43 CALMODULIN-BINDING.  
FT DOMAIN 192 500 CATALYTIC (BY SIMILARITY).  
FT VARSPIC 1 33 GSTATEELENTFKYLIGETEKWQRLKGI -> MDDH  
/FTID-VSP\_004546.  
FT CONFLICT 236 236 H -> G (IN REF. 4).  
FT CONFLICT 320 320 N -> W (IN REF. 4).  
SQ SEQUENCE 529 AA; 607112 MW; 24DB74C2A2A2AE06F CRC64;  
  
Query Match 59.5%; Score 1591.5; DB 1; Length 529;  
Best Local Similarity 61.2%; Pred. No. 8.4e-108;  
Matches 300; Conservative 91; Mismatches 90; Indels 9; Gaps 1;  
  
QY 19 LRYMYKQLENGEINTEELKKNLEYTASLLEAVYIDETQILDTDEQLRSDAYPSEVR 78  
DB 34 LRLCYKQLEKGVNVVIDLKKIEYAAVSLEAVYIDETRLDLDDELSQDSVPSEVR 93  
  
QY 79 DWLASTFTQARAKGRRAEKPFRSIVHVAQAGIFVERMPRTYTSVGYSTAVLNCL 138  
DB 94 DWLASTFTKMGKMMKKSEKPRFRSIVHVAQAGIFVERWKRSHVMGLAYPEAVITL 153  
  
QY 139 KNLDLWCDFVSLNQAADHALRTIVFELLTRHNLISRFKPTVFIMFLDALETGYGKY 198  
DB 154 KDVKWSEDFVFNALNEASGHSLSKFMVIELETRYDLINRKFIPVSLFAFALEAVGYSKY 213  
  
QY 199 KNPYHQNHAAADVTQVHCFLRTGCVHCLSEIELLAIIFAAAHIDYEHGTNTSFHIQT 258  
DB 214 KNPYHNLHAAADVTQVHYIMLHTGIMHWLTELILAMVFAAAHIDYEHGTNTSFHIQT 273

QY 259 KSECAIVYNDRSVLNHHISSVFLRMQDDENIFNLTKDEFVELRALVIEVLATDMSC 318  
DB 274 RSDVAILYNDRSVLNHHVSAAYRLMQDEENNVLINLSKDDWRDLNVLVIEVLSTDMSC 333  
  
QY 319 HFQVQVTKMTALQQLERIDKPKALSLLLHAADISHPTQKWLHVSHWTKALMEEPFRQGD 378  
DB 334 HFQVQIKNIRNSLQPEGLDKARTMSLILHAADISHPAKSWKLHHRWTALMEEPFLOGDK 393  
  
QY 379 EAEGLPSPICLDRSTLVAQSQIGFIDFIVEPTESVLTDVAEKSVQPLADEDSKKNOP 438  
DB 394 EAEGLPSPICLDRKSTVAQSQIGFIDFIVEPTESLTDSTEKIIILIEDSKTKTPS 453  
  
QY 439 SFQWRQPSLDVEVGD-----PNDVVSFRSTWVKRIQENKOKKERAASGTTNOMS 489  
DB 454 YGASRRSNMKGTTNDGTYSPOYSLASVDLKSFKNSLVDLIQNKERWELAAQGPDPHK 513  
  
QY 490 IDELSPCEEE 499  
DB 514 NSDLVNAEEK 523  
  
RESULT 9  
CNIA\_MOUSE STANDARD; PRT; 565 AA.  
ID CNIA\_MOUSE  
AC Q61481; O35388;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase  
DE 1A (EC 3.1.4.17) (Cam-PDE 1A) (61 kDa Cam-PDE).  
GN PDE1A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM PDE1A2).  
RC STRAIN=BALB/c; TISSUE=Brain;  
RA Yan C., Sonnenburg W.K., Zhao A.Z., Kwak K.S., Beavo J.A.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 1-262 FROM N.A. (ISOFORM PDE1A1).  
RC TISSUE=Heart;  
RA Sonnenburg W.K., Rybalkin S.D., Bornfeldt K.E., Kwak K.S.,  
RA Rybalkina I., Beavo J.A.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: HAS A HIGHER AFFINITY FOR CGMP THAN FOR CAMP.  
CC -!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -  
nucleoside 5'-phosphate.  
CC -!- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF  
CALMODULIN IN THE PRESENCE OF CA(2+).  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
Event-Alternative splicing; Named isoforms-2;  
Name=PDE1A2;  
IsoId=Q61481-1; Sequence=Displayed;  
Name=PDE1A1;  
IsoId=Q61481-2; Sequence=VSP\_004551;  
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
FAMILY.  
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DR EMBL; U56649; AAB03319.1; -;  
DR EMBL; AF023529; AAB81952.1; -;  
DR MGD; MGI:1201792; Pde1a.  
DR InterPro; IPR003607; Met\_phosphohydro.

```
DR InterPro: IPR002073; PDEase.
DR Pfam: PF00233; PDEase; 1
DR PRINTS: PR00287; PDIESTERASE1.
DR SMART: SM00471; HDC; 1.
DR PROSITE: PS00126; PDEASE_I; 1.
KW Hydrolase; CAMP; cAMP; Multigene family; Alternative splicing;
KW Calmodulin-binding.
FT DOMAIN 44 64 CALMODULIN-BINDING.
FT DOMAIN 213 535 MVGSSTSSSHVWAPRNITMGDTDIEELNATKYKILG
FT VARSPLIC 1 54 IQTEKMWRLKGI -> MDEVIVTRKKHLQRPFR (in
FT isoform PDE1A1).
FT /FTID=VSP_004551.
SQ SEQUENCE 565 AA; 64470 MW; 56A0749774967EE6 CRC64;
Query Match 58.98; Score 1575; DB 1; Length 565;
Best Local Similarity 60.48; Pred. No. 1.4e+106;
Matches 305; Conservative 85; Mismatches 91; Indels 24; Gaps 3;
QY 19 LRYMVKLENGEINIEELKNLEYTASLLAEVYIDETROIQLDTEDELOELRSDAVPSEVR 78
Db 55 LRLCVKLEKGDVNVVLDKKNIEYAAASVLEAVYIDETRRLLDTEDELSDIQTDSVPSEVR 114
QY 79 DNLASTFTQARAKGRAEKPRFRSTVHAVQAGIFVERMFRRTYTSVGPYTAIVNCL 138
Db 115 DNLASTFTRKGMGMKKPEEKPRFRSTVHAVQAGIFVERMYRKNYHMGVLTYPAAVITL 174
QY 139 KNLDLACDFVSLNQADHALTIVPELLTRNLISRKPIPTVFLMSDLALETGYK 198
Db 175 KEVDKNSFDVFNALNEASGSLKFMIVELFTRVDLNRKIPVPSCLIAFAEALEVGYSKH 234
QY 199 KNPYHNCIHAADYQVHCLELTGMVCHLSELELAIPAAIAHDEYHGTGNSPHIQ 258
Db 235 KNPYHNLVHAADYQVHYTLMHGIMHWELEILAWFPAIAHDEYHGTGNSPHIQ 294
QY 259 KSECAIVNDRSVLENHHSVRLQDDMMFINTKDEFVELRALVEMWLATDMSC 318
Db 295 RSDVAILNDRSVLENHHSVRLQDDMMFINTKDEFVELRALVEMWLATDMSC 354
QY 319 HFQOYKMTKALQOLERIDPKKALSLLLHAADISHTPKOWLHRSRTKALMEEFRRQDK 378
Db 355 HFQOIKRNSLQOPEGIDRAKTMSLILHAADISHPAKTWKLYRTMALMEEFRRQDK 414
QY 379 EAEGLPFPCLDRTSTLVASQSIGFIDFIVEPTFSLVDVAEKSVQPLADESKNQ- 437
Db 415 EAEGLPFPCLDRTSTLVASQSIGFIDFIVEPTFSLVDVAEKSVQPLADESKNQ- 474
QY 438 -----PSFQWROPSLDVEGDNP-----DVVSFRSTWVKRIQENKOK 475
Db 475 YGASSSTMTGPHVADSLRRSNTKSGVCDGSPADYSLSAVDLKFKNLVLDLIQNKER 534
QY 476 WKERAAG-ITNOMSDIELSPCEE 499
Db 535 WKELAAQGLDLHKNSEELGNTTEK 559
RESULT 10
CNIA_HUMAN
ID CNIA_HUMAN STANDARD; PRT; 534 AA.
AC R34750; Q9COK9; Q9COL3; Q9UFK3;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2003 (Rel. 42, Last annotation update)
DE Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase
DE 1A (EC 3.1.4.17) (Cam-PDE 1A) (61 kDa Cam-PDE) (hCam-1).
DE PDE1A.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=96132810; PubMed=8557689;
RA Loughney K., Martins T.J., Harris E.A.S., Sadhu K., Hicks J.B.,
RA Sonnenburg W.K., Beavo J.A., Ferguson K.;
RA "Isolation and characterization of cDNAs corresponding to two human
RA calcium, calmodulin-regulated, 3',5'-cyclic nucleotide
RA phosphodiesterases.";
RA J. Biol. Chem. 271:796-806(1996).
[2]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8 AND 9).
RP TISSUE=Heart;
RX MEDLINE=21240211; PubMed=11342109;
RA Michibata H., Yanaka N., Kanoh Y., Okumura K., Omori K.;
RA "Human Ca2+/calmodulin-dependent phosphodiesterase PDE1A: novel splice
RA variants, their specific expression, genomic organization, and
RA chromosomal localization.";
RA Biochim. Biophys. Acta 1517:278-287(2001).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP TISSUE=Brain;
RX MEDLINE=21614508; PubMed=11747989;
RA Fidoock M.D., Miller M., Lanfear J.;
RA "Isolation and differential tissue distribution of two human cDNAs
RA encoding PDE1 splice variants.";
RA Cell. Signal. 14:53-60(2002).
[4]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP TISSUE=Uterus;
RA Ottenwälder B., Obermaier B., Mewes H.-W., Gassenhuber J.,
RA Wiemann S.;
RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HAS A HIGHER AFFINITY FOR CAMP THAN FOR CAMP.
CC -!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -
CC nucleoside 5'-phosphate.
CC -!- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF
CC CALMODULIN IN THE PRESENCE OF CA(2+).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=9;
CC Name=1; Synonyms=PDE1A3, PDE1A6;
CC IscId=P54750-1; Sequence=Displayed;
CC Name=2; Synonyms=PDE1A4, PDE1A5;
CC IscId=P54750-2; Sequence=VSP_004547;
CC Name=3; Synonyms=PDE1A10;
CC IscId=P54750-3; Sequence=VSP_004548;
CC Name=4; Synonyms=PDE1A5;
CC IscId=P54750-4; Sequence=VSP_004549;
CC Name=5; Synonyms=PDE1A9;
CC IscId=P54750-5; Sequence=VSP_004550;
CC Name=6; Synonyms=PDE1A1;
CC IscId=P54750-6; Sequence=VSP_004549;
CC Name=7; Synonyms=PDE1A8;
CC IscId=P54750-7; Sequence=VSP_004547, VSP_004550;
CC Name=8; Synonyms=PDE1A11;
CC IscId=P54750-8; Sequence=VSP_004548, VSP_004549;
CC Name=9; Synonyms=PDE1A12;
CC IscId=P54750-9; Sequence=VSP_004548, VSP_004550;
CC -!- TISSUE SPECIFICITY: SEVERAL TISSUES, INCLUDING BRAIN, KIDNEY,
CC TESTIS, AND HEART.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U40370; AAC50436.1;
CC EMBL; AB038223; BAB20049.1;
CC EMBL; AB038208; BAB20049.1; JOINED.
CC EMBL; AB038211; BAB20049.1; JOINED.
CC EMBL; AB038213; BAB20049.1; JOINED.
```





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CC CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -
CC CC nucleoside 5'-phosphate.
CC CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC CC FAMILY. STRONG, TO MAMMALIAN TYPE 1 CAMP PHOSPHODIESTERASES.
CC CC -----
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CC CC or send an email to license@isb-sib.ch)
CC CC -----
CC CC EMBL: Z81114; CAB03289.1; -
CC CC PIR: T24459; T24459.
CC CC WormPep: T04D3.3; CE16340.
CC CC InterPro: IPRO03607; Met_phosphohydro.
CC CC InterPro: IPRO02073; PDEase.
CC CC Pfam: PF00233; PDEase; 1.
CC CC PRINTS: PR00387; PDIESTERASE1.
CC CC SMART: SM00471; HDC; 1.
CC CC PROSITE: PS00126; PDEASE_I; 1.
CC CC KW Hypothetical protein; Hydrolase; CGMP.
CC SQ SEQUENCE 664 AA; 74854 MW; 33436A301328201E CRC64;

Query Match 46.9%; Score 1254.5; DB 1; Length 664;
Best Local Similarity 47.0%; Pred. No. 2.9e-83;
Matches 255; Conservative 92; Mismatches 139; Indels 57; Gaps 11;

QY 8 QRSGLQPTIL-----RLRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETRIQLDTE 63
DB 138 KKSVDNAPALESEKRLYLHQLNSQLPLEDLKRNIYEAALVETPAYMDETRIGDEDD 197
QY 64 ELQELRSADVPSVRODLASTFTQQAARAKGRAEERKPFERSIVHVAQAGIFVERMRRY 123
DB 198 DLAEVTPETVPDEVREWLAAETFTQNAQKKR---DKPKFSVANARTGIFFEKLPKQ 254
QY 124 TSVGPTYSTAVLNCNLKLDLWCFVSLNQAADHALRTIVFELLTRHNLISRFKIPTVF 183
DB 255 VQOCP-IPPEIAELMEKVCVTSFPQLNEVSEGHAKYVGFELFNRYGFMDFKVPPLTA 313
QY 184 LMSFLDALETGYKYNPNYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLALIFAAAIH 243
DB 314 LENYLSALEVGYGSKHNNPNYHVAADVTQSSHFMLSOTGLANSLGDLLELAVLFGALII 373
QY 244 DYEGHTGTTNSFHIOKSECAIVYNDRSVLENHHISSVFRMLQDMMNFINLTKDFEVL 303
DB 374 DYEGHTGTTNHFHQSQSQFAMLYNDRSVLENHHVSSCFRLMKEDDKNLTHTLRDEYKEL 433
QY 304 RALVIEMLVATDMSCHFOQVKTMTALQOQLERIDKPKALSLLLHAADISHPTKQWLVHSR 363
DB 434 RNMVIEVLATDMSHTFMQTKTKMSLSLPEGIDKNKALCLIVHACDISHPAKPNLHER 493
QY 364 WTKALMEFPQGDKEAELGLPSPICDRSTSLVAOSQIGFIDFIVEPTFSVLTDVAES 423
DB 494 WTEGVLEFPQGDLEASMLGPYPSPICDRHTVHVSQIGFIDFIVEPTFVWVCGELLYVM 553
QY 424 VQPL-----ADEDS-----KKNQPSFQWROP-----SLDYE 450
DB 554 VEPVLSLPDTSFLPPSVQDGDKSPSNALSPLDLNRSSTSSSTRIRPLNVAKGLDI- 612
QY 451 VGDPNPDVFSRTWKRIQENKQKVKERAASGITNQMISDELSPCEEAPPSPADEHN 510
DB 613 ---PTP-----WMKFLHNKAHWKERAKE-EEERKKEAA--EAEAAAKQVE-ENK 657
QY 511 QNG 513
DB 658 ENG 660

RESULT 12
YST1_CABEL STANDARD; PRT; 549 AA.
ID YST1_CABEL

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Q22000:
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Probable 3',5'-cyclic phosphodiesterase R153.1 (EC 3.1.4.17).
R153.1.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Kirsten J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -
CC CC nucleoside 5'-phosphate.
CC CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC CC FAMILY. STRONG, TO MAMMALIAN TYPE 4 CAMP PHOSPHODIESTERASES.
CC CC -----
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CC CC or send an email to license@isb-sib.ch)
CC CC -----
CC CC EMBL: U28729; AAA68292.1; -
CC CC PIR: T16769; T16769.
CC CC WormPep: R153.1; CE02038.
CC CC InterPro: IPRO03607; Met_phosphohydro.
CC CC InterPro: IPRO02073; PDEase.
CC CC Pfam: PF00233; PDEase; 1.
CC CC PRINTS: PR00387; PDIESTERASE1.
CC CC SMART: SM00471; HDC; 1.
CC CC PROSITE: PS00126; PDEASE_I; 1.
CC CC KW Hypothetical protein; Hydrolase; CAMP.
CC SQ SEQUENCE 549 AA; 62904 MW; DF2EE6F03925DE87 CRC64;

Query Match 32.8%; Score 638; DB 1; Length 549;
Best Local Similarity 32.8%; Pred. No. 9.7e-39;
Matches 150; Conservative 89; Mismatches 157; Indels 62; Gaps 12;

QY 24 KQLENGEI-NIEELKKNLEYTASLLEAVYIDETRIQLDTEDELOELRSADVPSVRODLA 82
DB 118 RMLNKLSEHFARSSKGTQVSKFLITITMDKEDEPSIEI-----VPTEV----- 164
QY 83 SFTQQAARAKGRAEERKPFERSIVHVAQAGIF-----VERMFRRTVTSVGTSTAVLNC 137
DB 165 -----QCPSTSG-----PMTLSILKKAQTAAMNKISGVKLRAPSHDGHVPEYG--VNC 211
QY 138 -----LNKLDLWCFVSLNQAADHALRTIVFELLTRHNLISRFKIPTVFLMSFLDA 190
DB 212 AREIAVHMQELDDMGDPDFVKIDELSKNHSITVVTFSLLRQNLFKTFEIHQSTLVLYLN 271
QY 191 LETGYKYNPNYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLALIFAAAIHDEYHGT 250
DB 272 LEHHY--RNNHYHNEIHAADVAQSMHVLLMSPVLTEFVTLVLAIFAAGAVHDVDPGF 329
QY 251 TNSFHIOKSECAIVYNDRSVLENHHISSVFRMLQDMMNFINLTKDFEVLRAVLEM 310
DB 330 TNOYLINSNNELAIYNDSEVLEQHLAVAFKLLQDSNCFDLANLSRKQRLQRFKIVIM 389
QY 311 VLATDMSCHFOQVKTMTALQO-----LERI-DKPKALSLLLHAADISHPTKQWL 359
DB 390 VLATDMSKMSLLADLKTVMVAKKAGNANNVILVDKYNDRKIQVLSQSMHLDLSNPTKPIE 449
QY 360 VHSRWTKALMEFPQGDKEAELGLPSPICDRSTSLVAOSQIGFIDFIVEPTFSVLTDV 419
DB 450 LYQQMNRIMEYWRQGDKEKLEGLSEIPMCDRGNVTIEKSGVGFIDYIVHPLYETWADL 509
QY 420 AEKSVOPLADEDSKSNQPSFQWROPQPSLDVEGDPNPD 457

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Db 510 VYPDAQNILDQLEENR-----EWYQSRIPEE-----PD 537

Db 420 NSLHADVLGSHVLLATPALDAVFTDLELALFAAAIHVDVHGVSNQFLINTSELA 479  
Qy 264 IVYNDSEVLEHHISSVERLMODEMNIINLTKEFVELRALVIEWLATDMSCHFQV 323  
Db 480 LAYNDESVLEHHILANGVFLQGEHCIDFQNLKROSLKRWIDVMTLADMSKMTLL 539  
Qy 324 KTKMTALOOLE-----RIDPKALSLLLHAADISHPTKQWLIVSRWTKALMEEF 372  
Db 540 ADLKTWETKTKVTSVGVLNDYSDRIQVLRNMVHCADLSNPKPLEYLRQWTDRIMAEF 599  
Qy 373 FROGDEAEGLFPLCORTSTLVAQSQIGTFIDFIVEPTFSTVLTDAVKSVOPLAD--E 430  
Db 600 FQGDREEREMGEISPMCKDHTASVEKSOVGFIDYIVHPLWETWADLVHPDAQDILDTLE 659  
Qy 431 DSKS-----KNPSPFWQPSLDVEVG---DPN-PDVVSFRSTWTKRIQENKQWKERA 480  
Db 660 DNRDWHSAIRQSPS-----PTLEEPGVLSDPALPKFOFELT-----LEEEDEE----- 705  
Qy 481 ASGITNOMSIDELSPCEEAPPSP 504  
Db 706 -----DSLEVPGL-PCTEETLLAP 723

## RESULT 14

CN4C\_HUMAN STANDARD; PRT; 712 AA.  
ID CN4C\_HUMAN Q08493; Q9UN44; Q9UN45; Q9UN46; Q9UPJ6;  
AC Q08493; Q9UN44; Q9UN45; Q9UN46; Q9UPJ6;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 15-SEP-2003 (Rel. 42, Last annotation update)  
DE CAMP-specific 3',5'-cyclic phosphodiesterase 4C (EC 3.1.4.17)  
DE (PDE1) (PDE21).  
GN PDE4C.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM PDE4C1).  
RC TISSUE=Substantia nigra;  
RX MEDLINE=95145731; PubMed=7843419;  
RA Engels P., Sullivan M., Mueller T., Luebbert H.;  
RT "Molecular cloning and functional expression in yeast of a human  
RT CAMP-specific phosphodiesterase subtype (PDE IV-C).";  
RL FEBS Lett. 358:303-310(1995).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS PDE4C1; PDE4C2 AND PDE4C3).  
RX MEDLINE=20039485; PubMed=10574328;  
RA Sullivan M., Olsen A.S., Houslay M.D.;  
RT "genomic organisation of the human cyclic AMP-specific  
RT phosphodiesterase PDE4C gene and its chromosomal localisation to  
RT 19p13.1, between FAB3A and FUND.,"  
RL Cell. Signal. 11:735-742(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,  
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,  
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,  
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,  
RA Krommiller B., Arellano A., Saunders C., Ow D., Nolan M., Trong S.,  
RA Kobayashi A., Olsen A.S., Carrano A.V.;  
RT "Sequence analysis of an ~600 kb region in 19p13.1 between JAK3 and  
RT PDE4C.,"  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 462-712 FROM N.A.  
RX MEDLINE=94019330; PubMed=8413254;  
RA Bolger G., Michaeli T., Martins T., St John T., Steiner B.,  
RA Rodgers L., Riggs M., Wigler M., Ferguson K.;  
RT "A family of human phosphodiesterases homologous to the duncce

RT learning and memory gene product of Drosophila melanogaster are  
RT potential targets for antidepressant drugs.,"  
RL Mol. Cell. Biol. 13:6558-6571(1993).  
CC -|- CARALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O -  
CC adenosine 5'-phosphate.  
CC -|- ENZYME REGULATION: INHIBITED BY ROLIPRAM.  
CC -|- PATHWAY: Cyclic nucleotide metabolism.  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=7;  
CC Name=PDE4C1;  
CC IScID=Q08493-1; Sequence=Displayed;  
CC Name=PDE4C2;  
CC IScID=Q08493-2; Sequence=VSP\_004575;  
CC Name=PDE4C3;  
CC IScID=Q08493-3; Sequence=VSP\_004574;  
CC Name=PDE4C4;  
CC IScID=Q08493-4; Sequence=Not described;  
CC Name=PDE4C5;  
CC IScID=Q08493-5; Sequence=Not described;  
CC Name=PDE4C6;  
CC IScID=Q08493-6; Sequence=Not described;  
CC Name=PDE4C7;  
CC IScID=Q08493-7; Sequence=Not described;  
CC -|- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES BUT NOT IN CELLS  
CC OF THE IMMUNE SYSTEM.  
CC -|- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
CC FAMILY.  
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CC -----  
CC EMBL: Z45632; CA86601.1;  
CC EMBL: AF157816; AAD47053.1;  
CC EMBL: AF157813; AAD47053.1; JOINED.  
CC EMBL: AF157814; AAD47053.1; JOINED.  
CC EMBL: AF157815; AAD47053.1; JOINED.  
CC EMBL: AF157816; AAD47054.1;  
CC EMBL: AF157817; AAD47054.1; JOINED.  
CC EMBL: AF157818; AAD47054.1; JOINED.  
CC EMBL: AF157819; AAD47054.1; JOINED.  
CC EMBL: AF157820; AAD47054.1; JOINED.  
CC EMBL: AF157821; AAD47055.1;  
CC EMBL: AF157822; AAD47055.1; JOINED.  
CC EMBL: AF157823; AAD47055.1; JOINED.  
CC EMBL: AF157824; AAD47055.1; JOINED.  
CC EMBL: AF157825; AAD47055.1; JOINED.  
CC EMBL: AF157826; AAD47055.1; JOINED.  
CC EMBL: AF157827; AAD47055.1; JOINED.  
CC EMBL: AF157828; AAD47055.1; JOINED.  
CC EMBL: AF157829; AAD47055.1; JOINED.  
CC EMBL: AF157830; AAD47055.1; JOINED.  
CC EMBL: AF157831; AAD47055.1; JOINED.  
CC EMBL: AF157832; AAD47055.1; JOINED.  
CC EMBL: AF157833; AAD47055.1; JOINED.  
CC EMBL: AF157834; AAD47055.1; JOINED.  
CC EMBL: AF157835; AAD47055.1; JOINED.  
CC EMBL: AF157836; AAD47055.1; JOINED.  
CC EMBL: AF157837; AAD47055.1; JOINED.  
CC EMBL: AF157838; AAD47055.1; JOINED.  
CC EMBL: AF157839; AAD47055.1; JOINED.  
CC EMBL: AF157840; AAD47055.1; JOINED.  
CC EMBL: AF157841; AAD47055.1; JOINED.  
CC EMBL: AF157842; AAD47055.1; JOINED.  
CC EMBL: AF157843; AAD47055.1; JOINED.  
CC EMBL: AF157844; AAD47055.1; JOINED.  
CC EMBL: AF157845; AAD47055.1; JOINED.  
CC EMBL: AF157846; AAD47055.1; JOINED.  
CC EMBL: AF157847; AAD47055.1; JOINED.  
CC EMBL: AF157848; AAD47055.1; JOINED.  
CC EMBL: AF157849; AAD47055.1; JOINED.  
CC EMBL: AF157850; AAD47055.1; JOINED.  
CC EMBL: AF157851; AAD47055.1; JOINED.  
CC EMBL: AF157852; AAD47055.1; JOINED.  
CC EMBL: AF157853; AAD47055.1; JOINED.  
CC EMBL: AF157854; AAD47055.1; JOINED.  
CC EMBL: AF157855; AAD47055.1; JOINED.  
CC EMBL: AF157856; AAD47055.1; JOINED.  
CC EMBL: AF157857; AAD47055.1; JOINED.  
CC EMBL: AF157858; AAD47055.1; JOINED.  
CC EMBL: AF157859; AAD47055.1; JOINED.  
CC EMBL: AF157860; AAD47055.1; JOINED.  
CC EMBL: AF157861; AAD47055.1; JOINED.  
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CC EMBL: AF158172; AAD4705





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2003, 00:48:06 ; Search time 70 seconds  
(without alignments)  
1902.216 Million cell updates/sec

Title: US-09-663-481-1  
Perfect score: 2676  
Sequence: 1 MANPVPVQSHLQGPILRLR.....EEAPPSPAEDHNQNGNLD 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp.archaea:\*
- 2: sp.bacteria:\*
- 3: sp.fungi:\*
- 4: sp.human:\*
- 5: sp.invertebrate:\*
- 6: sp.mammal:\*
- 7: sp.mhc:\*
- 8: sp.organelle:\*
- 9: sp.phage:\*
- 10: sp.plant:\*
- 11: sp.rodent:\*
- 12: sp.virus:\*
- 13: sp.vertibrate:\*
- 14: sp.unclassified:\*
- 15: sp.virus:\*
- 16: sp.bacteriap:\*
- 17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2676	100.0	516	4 Q96KP3	Q96kp3 homo sapien
2	2349	95.3	536	6 Q9BE16	Q9be16 macaca fasc
3	2473	92.4	495	11 Q9DBS6	Q9db56 mus musculu
4	1626.5	60.8	515	6 Q95NB8	Q95nb8 canis famli
5	1618	60.5	529	4 Q9C0L0	Q9c010 homo sapien
6	1616.5	60.4	536	4 Q9C0L4	Q9c014 homo sapien
7	1595	59.6	603	11 Q8CDV2	Q8cdv2 mus musculu
8	1593	59.6	706	11 Q8BSV6	Q8bsv6 mus musculu
9	1593	59.5	617	11 Q9DSW0	Q9dsw0 mus musculu
10	1589	59.5	634	4 Q8TAE4	Q8tae4 homo sapien
11	1589	59.4	769	4 Q8NB10	Q8nb10 homo sapien
12	1575	58.9	545	11 Q8BR9	Q8br9 mus musculu
13	1551.5	58.0	542	11 Q9EP9	Q9ep9 rattus norv
14	1432	53.5	511	4 Q9C0K8	Q9c0k8 homo sapien
15	1431.5	53.5	456	11 Q9JL19	Q9jll9 mus musculu
16	1430.5	53.5	518	4 Q9C0L2	Q9c0l2 homo sapien

17	1424.5	53.2	501	4 Q9C0L1	Q9c0l1 homo sapien
18	1149.5	43.0	605	5 Q9VKE9	Q9vke9 drosophila
19	1143.5	42.7	834	5 Q8XRO	Q8xro drosophila
20	999	37.3	199	11 Q64395	Q64395 cricetus
21	948	35.4	184	4 Q16713	Q16713 homo sapien
22	855	32.0	628	5 Q96075	Q96075 ephydatia f
23	638	23.8	599	5 Q8IF23	Q8if23 caenorhabdi
24	638	23.8	626	5 Q952Q6	Q952q6 caenorhabdi
25	631	23.6	700	4 P78505	P78505 homo sapien
26	630	23.5	782	4 Q76105	Q76105 homo sapien
27	630	23.5	791	4 Q43849	Q43849 homo sapien
28	629	23.5	518	4 Q43850	Q43850 homo sapien
29	622.5	23.3	584	11 Q8C4Q7	Q8c4q7 mus musculu
30	622.5	23.3	771	11 Q9EQR7	Q9eqr7 rattus norv
31	622	23.2	426	4 Q9UPJ5	Q9upj5 homo sapien
32	617.5	23.1	518	4 Q8IVD3	Q8ivd3 homo sapien
33	617.5	23.1	748	4 Q8IVD2	Q8ivd2 homo sapien
34	617	23.1	521	5 Q8MRN3	Q8mrn3 drosophila
35	617	23.1	624	5 Q9W4S8	Q9w4s8 drosophila
36	617	23.1	629	5 Q8IRU5	Q8iru5 drosophila
37	617	23.1	642	5 Q8IRU6	Q8iru6 drosophila
38	617	23.1	662	5 Q8IRU4	Q8iru4 drosophila
39	617	23.1	711	5 Q8IRU7	Q8iru7 drosophila
40	617	23.1	776	5 Q8IRU8	Q8iru8 drosophila
41	617	23.1	778	5 Q8IRU9	Q8iru9 drosophila
42	617	23.1	1070	5 Q8IRV0	Q8irv0 drosophila
43	617	23.1	1209	5 Q8MS17	Q8ms17 drosophila
44	617	23.1	1209	5 Q8IRV1	Q8irv1 drosophila
45	616.5	23.0	687	4 Q8IV84	Q8iv84 homo sapien

#### ALIGNMENTS

#### RESULT 1

Q96KP3 PRELIMINARY; PRT; 516 AA.  
AC Q96KP3;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE 3/5' cyclic nucleotide phosphodiesterase 1B2.  
GN PDE1B2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Tissue-Testis;  
RA Fidock M.D., Miller M., Lanfear J.;  
RT "Isolation and differential tissue distribution of two human cDNAs encoding PDE1 splice variants."  
RL "Cell. Signal. 14:53-60(2001)."  
DR EMBL; AJ401609; CAC82207.1;  
DR InterPro; IPR003607; Met.phosphohydro.  
DR InterPro; IPR002073; PDEase.  
DR Pfam; PF00233; PDEase; 1.  
DR PRINTS; PR00387; PD1ESTERASE1.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDEASE-1; 1.  
SQ SEQUENCE 516 AA: 59051 MW; 0A9093462479DC5C CRC64;

Query Match 100.0%; Score 2676; DB 4; Length 516;  
Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANPVPVQSHLQGPILRLRWVKOLENGEINIEELKKNLEYTASLLSEAVYIDETQRLD 60  
Db 1 MANPVPVQSHLQGPILRLRWVKOLENGEINIEELKKNLEYTASLLSEAVYIDETQRLD 60  
QY 61 TEDELQELRSDAVPSEVRDNLASTTQQAARAKGRAEKKPKFRSVHVAQAGIFVERMFR 120  
|||||

Db 61 TEDELQELSDAVPSEVRDLASTFTQQAARAGRRAEKPKERSIVHVAQAGIFVERMER 120  
 QY 121 RYTVSGPYSTAVLNCNLDWCDDVSLNQADDDHALRTIVFELLTRHNLISRFKIP 180  
 Db 121 RYTVSGPYSTAVLNCNLDWCDDVSLNQADDDHALRTIVFELLTRHNLISRFKIP 180  
 QY 181 TVFLMSFLDALETGYGKYKNPNHNOIHAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAA 240  
 Db 181 TVFLMSFLDALETGYGKYKNPNHNOIHAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAA 240  
 QY 241 AIHDEHTGTTNSFHIOQSECAIYVNDRSVLNHHISSVFRMLQDDENNFINTKDF 300  
 Db 241 AIHDEHTGTTNSFHIOQSECAIYVNDRSVLNHHISSVFRMLQDDENNFINTKDF 300  
 QY 301 VELRALVIMVLATDMSCHFSQVQVTKMTALQQLERIDKPKALSLLLHAADISHPTKQWLV 360  
 Db 301 VELRALVIMVLATDMSCHFSQVQVTKMTALQQLERIDKPKALSLLLHAADISHPTKQWLV 360  
 QY 361 HSRWTKALMEEFPROGDKAEELGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVA 420  
 Db 361 HSRWTKALMEEFPROGDKAEELGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVA 420  
 QY 421 EKSVOPLADEDSKSNOPSFQWRQPSLDVEGDPNDVVSFRSTWVKRIQENKQWKERA 480  
 Db 421 EKSVOPLADEDSKSNOPSFQWRQPSLDVEGDPNDVVSFRSTWVKRIQENKQWKERA 480  
 QY 481 ASGITNOMSIDELSPCEEAPPSPAEDEHNQNLID 516  
 Db 481 ASGITNOMSIDELSPCEEAPPSPAEDEHNQNLID 516

## RESULT 2

Q9BSE6 PRELIMINARY; PRT; 536 AA.  
 AC Q9BSE6  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypochemical 61.4 kDa protein.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
 OC Cercopitheidae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Frontal cortex;  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
 RA Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA  
 RT libraries";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB060237; BAB41164.1;  
 DR InterPro; IPR003607; Met\_phosphohydro.  
 DR InterPro; IPR002073; PDEase.  
 DR Pfam; PF00233; PDEase.1.  
 DR PRINTS; PR00387; PDIERASE1.  
 DR SMART; SM00471; HDC; 1.  
 DR PROSITE; PS00126; PDEASE\_I; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 536 AA; 61364 MW; 5B0F82829574B9C6 CRC64;

Query Match 95.3%; Score 2549; DB 6; Length 536;  
 Best Local Similarity 98.0%; Pred. No. 4.6e-196;  
 Matches 488; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 19 LRYMKVQLENGEINTIEELKKNLEYTASLEAVYIDETQILDTEDELQELSDAVPSEVR 78  
 Db 39 LRYMKVQLENGEINTIEELKKNLEYTASLEAVYIDETQILDTEDELQELSDAVPSEVR 98  
 QY 79 DMLASTFTQQAARAGRRAEKPKERSIVHVAQAGIFVERMERFTYTSVGYTSTAVLNCL 138  
 Db 99 DMLASTFTQQAARAGRRAEKPKERSIVHVAQAGIFVERMERFTYTSVGYTSTAVLNCL 158

QY 139 KNLDWCDDVSLNQADDDHALRTIVFELLTRHNLISRFKIP 198  
 Db 139 KNLDWCDDVSLNQADDDHALRTIVFELLTRHNLISRFKIP 198  
 QY 199 KNPYHNOIHAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAAIHDYEHGTGTSNFHIQT 258  
 Db 219 KNPYHNOIHAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAAIHDYEHGTGTSNFHIQT 278  
 QY 259 KSECAIYVNDRSVLNHHISSVFRMLQDDENNFINTKDFEVLRALVIMVLATDMS 318  
 Db 279 KSECAIYVNDRSVLNHHISSVFRMLQDDENNFINTKDFEVLRALVIMVLATDMS 338  
 QY 319 HFQVQVTKMTALQQLERIDKPKALSLLLHAADISHPTKQWLVHSRWTKALMEEFPROGDK 378  
 Db 339 HFQVQVTKMTALQQLERIDKPKALSLLLHAADISHPTKQWLVHSRWTKALMEEFPROGDK 398  
 QY 379 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKSNOP 438  
 Db 399 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKSNOP 458  
 QY 439 SFQWRQPSLDVEGDPNDVVSFRSTWVKRIQENKQWKERAASGITNOMSIDELSPCEE 498  
 Db 459 SFQWRQPSLDVEGDPNDVVSFRSTWVKRIQENKQWKERAASGITNOMSIDELSPCEE 518  
 QY 499 EAPPSPADEHNQNLID 516  
 Db 519 EAPPSPADEHNQNLID 536

## RESULT 3

Q9DBS6 PRELIMINARY; PRT; 495 AA.  
 AC Q9DBS6  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Adult male lung cDNA, RIKEN full-length enriched library,  
 DE clone:12J0014008, full insert sequence.  
 GN PDE1B OR PDE1B1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Lung;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarcs P.,  
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki E., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki E., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 DR EMBL; AF004772; BAB23551.1;  
 DR MGD; MGI:97523; Pde1b.  
 DR InterPro; IPR003607; Met\_phosphohydro.  
 DR InterPro; IPR002073; PDEase.  
 DR Pfam; Pf00233; PDEase; 1.



DR PRINTS; PR00387; PD1ESTERASE1.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDEASE\_I; 1.  
SQ SEQUENCE 495 AA; 56598 MW; FB86B38967CFD0C4 CRC64;

Query Match 92.4%; Score 2473; DB 11; Length 495;  
Best Local Similarity 95.8%; Pred. No. 5.2e-190;  
Matches 474; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 22 MVKOLENGEINIEELKKNLEYTASLLEAVYIDETQRIIDTEDEQLERSDAVPSEVRDL 81  
DB 1 MVKOLENGEVNIEELKKNLEYTASLLEAVYIDETQRIIDTEDEQLERSDAVPSEVRDL 60  
QY 82 ASTTQARAKGRAEERPKERSIVHVAQAGIFVERMERRTYTSVGPYTSVAVLNCKNL 141  
DB 61 ASTTQOTRAGRAREERPKERSIVHVAQAGIFVERMERRTYTSVGPYTSVAVLNCKNL 120  
QY 142 DLWCFDVFSLNQAADHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGKGKYNP 201  
DB 121 DLWCFDVFSLNQAADHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGKGKYNP 180  
QY 202 YHNOIHAADVTQVHCFLRGMVHCSEIELLAIIFAAAHDEYHGTGTTNSFHIQKSE 261  
DB 181 YHNOIHAADVTQVHCFLRGMVHCSEIELLAIIFAAAHDEYHGTGTTNSFHIQKSE 240  
QY 262 CAIYVNDRLSVLENHHSVFLMQDDENNIPTKDEFVELRALVIEMLATDMSCHFQ 321  
DB 241 CAIYVNDRLSVLENHHSVFLMQDDENNIPTKDEFVELRALVIEMLATDMSCHFQ 300  
QY 322 QVTKMTALQOLERIDKPKALSLLLHAADI SHPTKQWLVHRSWKALMEEFROGDKAE 381  
DB 301 QVTKMTALQOLERIDKPKALSLLLHAADI SHPTKQWLVHRSWKALMEEFROGDKAE 360  
QY 382 LGLPESPLCDRTSTLVAOSQIGFDFIVEPTFSLTVAESVQPLADESKSNQPSFQ 441  
DB 361 LGLPESPLCDRTSTLVAOSQIGFDFIVEPTFSLTVAESVQPLADESKSNQPSFQ 420  
QY 442 WRQPSLDVEGDPNPVYFSTRSTWKRIQENKQKWKERAAAGITNQMSIDELSPCEEAP 501  
DB 421 WRQPSLDVVDGPNPVDVYFSTRATWKYIQENKQKWKERAAAGITNQMSIDELSPCEEAP 480  
QY 502 PSPAEDHNQNGNLD 516  
DB 481 SSPAEDHNQNGNLD 495

RESULT 4

Q95NB8 PRELIMINARY; PRT; 515 AA.  
AC Q95NB8;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Calmodulin-activated cyclic nucleotide phosphodiesterase.  
GN PDE1A.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21261952; PubMed=11368912;  
RA Clapham J.C., Wilderspin A.F.;  
RT "Cloning of dog heart PDE1A, a first detailed characterization at the  
molecular level in this species.";  
RL Gene 268:165-171(2001).  
DR EMBL; AF252536; AAK39971.1; -  
DR InterPro; IPR003607; Met\_phsphohydro.  
DR Pfam; PF00233; PDEase; 1.  
DR PRINTS; PR00387; PD1ESTERASE1.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDEASE\_I; 1.

SQ SEQUENCE 515 AA; 59374 MW; BE41DBBBFC1DCC2A CRC64;

Query Match 60.8%; Score 1626.5; DB 6; Length 515;  
Best Local Similarity 62.2%; Pred. No. 4.7e-122;  
Matches 306; Conservative 90; Mismatches 8; Indels 9; Gaps 1;

QY 1 MANPVQVORSHLQGPILRLRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETQRIID 60  
DB 1 MDDHVTIRKKHLQRFIFRLCLVQLERGDVNVVDLKKNIEVAAASLEAVYIDETRLLD 60  
QY 61 TEDELQEURSDAVPSEVRDLASTTQARAKGRAEERPKERSIVHVAQAGIFVERMER 120  
DB 61 TEDELSDIQTDSPSEVRDLASTTFRKGMKMMKKSEKPKERSIVHVAQAGIFVERMYR 120  
QY 121 RYTSVSGPTYSTAVLNCKNLDLWCFDVFSLNQAADHALRTIVFELLTRHNLISRFKIP 180  
DB 121 KSYHMGVLVYPEAVITLKDVKDSFDFALNEASGEHSLKPMIYELFTRDILNRFKIP 180  
QY 181 TVFLMSFLDALETGKGKYNPYHNOIHAADVTQVHCFLRGMVHCSEIELLAIIFAA 240  
DB 181 VSCLISFAEAEVGYSKYKPNYHNLHAADVTQVHYIMLHTGINHMLTELEILAWVFAA 240  
QY 241 AIHDYHGTGTTNSFHIQKSECAIYVNDRLSVLENHHSVFLMQDDENNIPTKDEF 300  
DB 241 AIHDYHGTGTTNSFHIQKSECAIYVNDRLSVLENHHSVFLMQDDENNIPTKDEF 300  
QY 301 VELRALVIEMLATDMSCHFQVTKMTALQOLERIDKPKALSLLLHAADISHPTKQWLV 360  
DB 301 RDLRLVIEMLVSTDMSCHFOQIKNRNSLQOPEGIDKAKTMSLILHAADISHPAKSNQL 360  
QY 361 HSRWTALMEEFROGDKAEELGFLPSPCLDRTSTLVAOSQIGFDFIVEPTFSLTVA 420  
DB 361 HYRTMALMEEFROGDKAEELGFLPSPCLDRTSTLVAOSQIGFDFIVEPTFSLTVA 420  
QY 421 EKSQVPLADESKSNQPSFQWRQPSLDVEGDD-----PNPDVYFSTRSTWKRIQ 471  
DB 421 EKIIPLTEEASKTDTSSYGASRRSNMKGTMNDGTSPDYSVLASVLDKSFKNLVDIIQQ 480  
QY 472 NKQWKERAAAG 483  
DB 481 NKERKELAAAG 492

RESULT 5

Q9COL0 PRELIMINARY; PRT; 529 AA.  
AC Q9COL0;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Calmodulin-dependent phosphodiesterase.  
GN HSPDE1A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21240211; PubMed=11342109;  
RA Michibata H., Yanaka N., Kanoh Y., Okumura K., Omori K.;  
RT "Human Ca2+/calmodulin-dependent phosphodiesterase PDE1A: novel splice  
variants, their specific expression, genomic organization, and  
chromosomal localization.";  
RL Biochim. Biophys. Acta 1517:278-287(2001).  
DR EMBL; AB038224; BAB20055.1; -  
DR EMBL; AB038208; BAB20055.1; JOINED.  
DR EMBL; AB038211; BAB20055.1; JOINED.  
DR EMBL; AB038213; BAB20055.1; JOINED.  
DR EMBL; AB038214; BAB20055.1; JOINED.  
DR EMBL; AB038215; BAB20055.1; JOINED.  
DR EMBL; AB038216; BAB20055.1; JOINED.  
DR EMBL; AB038217; BAB20055.1; JOINED.  
DR EMBL; AB038218; BAB20055.1; JOINED.



RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=Testis;  
RC MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
DR EMBL; AK029531; BAC26499.1; -;  
SQ SEQUENCE 603 AA; 68348 MW; 4561AC1AF2FBCF47 CRC64;

Query Match 59.6%; Score 1595; DB 11; Length 603;  
Best Local Similarity 60.5%; Pred. No. 1.9e-119;  
Matches 310; Conservative 81; Mismatches 81; Indels 40; Gaps 5;

QY 18 RLRYVMVKOLENGEINIEELKKNLKLEYTASLLKLEYIDETROILDTDELEQLRSDAVPSEV 77  
DB 15 RLRLSVKOLENGEASVDLKKNLKLEYAATVLESVYIDETRRLLDYELELSDIQSDAVPSEV 74  
QY 78 RDWLASTFTQOARAKRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPITYSTAVLNC 137  
DB 75 RDWLASTFTQMGMLRRSDEKPRKSIHVAQAGIFVERMYRTSNMVGLSYPPAVIDA 134  
QY 138 LKNLDLWCFVFSLNQAADHALRTIVFELLTRHNLISRFKIPITVFLMSFLDALETGYGK 197  
DB 135 LKQVDVTSFDFVSLNEASGDHALKFIFYELLTRYDLISRFPKIPISALVSFVEALEVGYK 194  
QY 198 YKNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIDHYEHTGTTNSFHQ 257  
DB 195 HKNPYHNLHMAADVTQTVHYLLYKTGVANWLTELEIFAIIFSAALHDEYHTGTTNNFHQ 254  
QY 258 TKSECAIYNDRSVLENHHSVFRMQ-DDEMNIFINLTDEFEVLRALVEMVLATDM 316  
DB 255 TRSDPAIYNDRSVLENHLSAAVRLQDEEMNLVNSKDDNREFRTLVIEMVATDM 314  
QY 317 SCHFOQVTKMTALQOOLERIDPKKALSLLLHAADISHPTKOWLVHSRWTKALMEEFRRQ 376  
DB 315 SCHFOQIKAMTKALQOPEAIEPKKALSLMLHTADISHPAKAWDLHRRWTMSLLEEFFRQ 374  
QY 377 DKEALGLPFPSPCLDRSTLVAQSQIGFDIVPTFVTSVLTDAEKSQVQPLADEDSKSN 436  
DB 375 DREALGLPFPSPCLDRKSTWVAQSQVGFIDFIVEPTFTVLTDMTEKIVSPLIDESSQTGG 434  
QY 437 QPSFQWRQPSLD-VEVGDPN-----PDVVSFRSTWVKRIQENKQ 474  
DB 435 TQQ---RRSSLNSINSDAKRGVKSQSGSDGAPINNSVIPVDYKSKFATWTEVVQINRE 491  
QY 475 KWKEAASGINTQMSIDELSCPEEAPPSPAE 506  
DB 492 RWRKV-----PKEAKKAEAE 509

RESULT 8  
QB8SV6  
ID QB8SV6 PRELIMINARY; PRT; 706 AA.  
AC QB8SV6;  
DT 01-MAR-2003 (TremBLrel. 23, Created)  
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Phosphodiesterase 1C.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=Pituitary;  
RC MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).

DR EMBL; AK030423; BAC26956.1; -;  
SQ SEQUENCE 706 AA; 80290 MW; 1F58533E1259801F CRC64;

Query Match 59.6%; Score 1595; DB 11; Length 706;  
Best Local Similarity 60.5%; Pred. No. 2.4e-119;  
Matches 310; Conservative 81; Mismatches 81; Indels 40; Gaps 5;

QY 18 RLRYVMVKOLENGEINIEELKKNLKLEYTASLLKLEYIDETROILDTDELEQLRSDAVPSEV 77  
DB 43 RLRLSVKOLENGEASVDLKKNLKLEYAATVLESVYIDETRRLLDYELELSDIQSDAVPSEV 102  
QY 78 RDWLASTFTQOARAKRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPITYSTAVLNC 137  
DB 103 RDWLASTFTQMGMLRRSDEKPRKSIHVAQAGIFVERMYRTSNMVGLSYPPAVIDA 162  
QY 138 LKNLDLWCFVFSLNQAADHALRTIVFELLTRHNLISRFKIPITVFLMSFLDALETGYGK 197  
DB 163 LKQVDVTSFDFVSLNEASGDHALKFIFYELLTRYDLISRFPKIPISALVSFVEALEVGYK 222  
QY 198 YKNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIDHYEHTGTTNSFHQ 257  
DB 223 HKNPYHNLHMAADVTQTVHYLLYKTGVANWLTELEIFAIIFSAALHDEYHTGTTNNFHQ 282  
QY 258 TKSECAIYNDRSVLENHHSVFRMQ-DDEMNIFINLTDEFEVLRALVEMVLATDM 316  
DB 283 TRSDPAIYNDRSVLENHLSAAVRLQDEEMNLVNSKDDNREFRTLVIEMVATDM 342  
QY 317 SCHFOQVTKMTALQOOLERIDPKKALSLLLHAADISHPTKOWLVHSRWTKALMEEFRRQ 376  
DB 343 SCHFOQIKAMTKALQOPEAIEPKKALSLMLHTADISHPAKAWDLHRRWTMSLLEEFFRQ 402  
QY 377 DKEALGLPFPSPCLDRSTLVAQSQIGFDIVPTFVTSVLTDAEKSQVQPLADEDSKSN 436  
DB 403 DREALGLPFPSPCLDRKSTWVAQSQVGFIDFIVEPTFTVLTDMTEKIVSPLIDESSQTGG 462  
QY 437 QPSFQWRQPSLD-VEVGDPN-----PDVVSFRSTWVKRIQENKQ 474  
DB 463 TQQ---RRSSLNSINSDAKRGVKSQSGSDGAPINNSVIPVDYKSKFATWTEVVQINRE 519  
QY 475 KWKEAASGINTQMSIDELSCPEEAPPSPAE 506  
DB 520 RWRKV-----PKEAKKAEAE 537

RESULT 9  
QB5D5W0  
ID QB5D5W0 PRELIMINARY; PRT; 617 AA.  
AC QB5D5W0;  
DT 01-JUN-2001 (TremBLrel. 17, Created)  
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Adult male testis cDNA, RIKEN full-length enriched library,  
DE clone:4921514B09, full insert sequence (Phosphodiesterase 1C).  
GN PDE1C.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=Testis;  
RC MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP NCBI\_TaxID=9606;  
SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,  
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,  
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,  
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,  
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kenehori K.,  
RA Takahashi-Fuji A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,  
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,  
RT "NEO human cDNA sequencing project."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AK091734; BAC03734.1; -  
DR InterPro: IPR003607; Met\_phosphohydro.  
DR InterPro: IPR002073; PDEase.  
DR Pfam: PF00233; PDEase; 1.  
DR PRINTS: PRO0387; PDIESTERASE1.  
DR SMART: SM00471; HDC; 1.  
DR PROSITE: PS00126; PDEASE\_I; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 769 AA; 86910 MW; CEB8E7FC05B6CED1 CRC64;  
  
Query Match 59.4%; Score 1589; DB 4; Length 769;  
Best Local Similarity 60.7%; Pred. No. 8.1e-119;  
Matches 311; Conservative 78; Mismatches 83; Indels 40; Gaps 5;  
  
QY 18 LRVMVVKQLENGEINIEELKKNLEYTASLLEAVYIDETROIILDTDEQLRSDAVPSEV 77  
DB 103 LRLSVLKQLENGEASVVDLKNLEYAATVLESVYIDETRLRLDTDELSIQSDAVPSEV 162  
  
QY 78 RDLASTFTQOARAKRAEERPKFRSIVHVAQAGIFVERMFRRTYTSVGPYSAVLNC 137  
DB 163 RDLASTFTQGMRLRSDERPLFKSIVHVAQAGIFVERMFRRTYTSVGPYSAVLNC 222  
  
QY 138 LKNLDLWCFDVSFLNQAAADHALRTIVFELLTRHNLISRFKTIPTVFLMSFLDALETGYK 197  
DB 223 LKVDKWSFDFVSLNEASGDHALKTFYELLTRYDLISRFKIPISALVSFVALEVGYSK 282  
  
QY 198 KNPYHNQIHAADVDTQVHCFLRTGMVHCLSEIELLAIIFAAAIHDYHTGTTNSFHQ 257  
DB 283 KNPYHNLMHAADVDTQVHYLLKTVGANWLTETELFAIFSAAIHDYHTGTTNFHIQ 342  
  
QY 258 TKSECAIVYNDRSVLNHHISSVFLMODD-EMNIFINLTDFEVELRALVIEVMYATDM 316  
DB 343 TRSDPAIYNDRSVLNHHLSAAYRLQDDEEMNILNLSKDDWREFRFLVIEVMYATDM 402  
  
QY 317 SCHFOQVKMTALQQLERIDKPKALSLLLHAADISHPTKQWLHVRWTKALMEEFFRQ 376  
DB 403 SCHFOQIRAKMTALQOPEAIEKPKALSLMLHTADISHPAKAWDLHRTWMSLLEEFFRQ 462  
  
QY 377 DREAELGLPFPCLDRTSTLVAQSOIGFDIFVEPTFSLTDAEKSQVPLADEDSKSN 436  
DB 463 DREAELGLPFPCLDRKSTWVAQSOVGFDIFVEPTFSLTDAEKSQVPLADEDSQSG 522  
  
QY 437 QFSFQWRQPSLD-VEVGDP-----NPDVVSFRSTWVKRQENKQ 474  
DB 523 TCQ---RRSLNLSISSDAKRSVKTSSEGSAPINNVSIVDYKSFRTATWTEVVRHNE 579  
  
QY 475 WKERAASGITNOMSIDELSPCEEPAPPSPAE 506  
DB 580 RWRKV-----PKEAKKEAEE 597  
  
RESULT 12  
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AC Q8BRR9;  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

DE Phosphodiesterase 1A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cortex;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
DR EMBL: AK043647; BAC31606.1; -  
SQ SEQUENCE 545 AA; 62347 MW; 5B79AC8DE8456917 CRC64;  
  
Query Match 58.9%; Score 1575; DB 11; Length 545;  
Best Local Similarity 60.4%; Pred. No. 6.8e-118;  
Matches 305; Conservative 85; Mismatches 91; Indels 24; Gaps 3;  
  
QY 19 LRVMVVKQLENGEINIEELKKNLEYTASLLEAVYIDETROIILDTDEQLRSDAVPSEV 78  
DB 35 LRLSVLKQLENGEASVVDLKNLEYAATVLESVYIDETRLRLDTDELSIQSDAVPSEV 94  
  
QY 79 DRLASTFTQOARAKRAEERPKFRSIVHVAQAGIFVERMFRRTYTSVGPYSAVLNCL 138  
DB 95 DRLASTFTKMKGMKKKPEEKPKFRSIVHVAQAGIFVERMFRRTYTSVGPYSAVLNCL 154  
  
QY 139 LKNLDLWCFDVSFLNQAAADHALRTIVFELLTRHNLISRFKTIPTVFLMSFLDALETGYK 198  
DB 155 KVDKWSFDFVSLNEASGDHALKTFYELLTRYDLINRFPKIPVSCLIAPAEALEVGYSK 214  
  
QY 199 KNPYHNQIHAADVDTQVHCFLRTGMVHCLSEIELLAIIFAAAIHDYHTGTTNSFHQ 258  
DB 215 KNPYHNLMHAADVDTQVHYLLKTVGANWLTETELFAIFSAAIHDYHTGTTNFHIQ 274  
  
QY 259 TKSECAIVYNDRSVLNHHISSVFLMODD-EMNIFINLTDFEVELRALVIEVMYATDMSC 318  
DB 275 RSDVAILYNDRSVLNHHVSAAYRLMOEEMILNLSKDDWRDLNVLNVLATDMSC 334  
  
QY 319 HFQOQVKMTALQQLERIDKPKALSLLLHAADISHPTKQWLHVRWTKALMEEFFRQ 378  
DB 335 HFQOQKINRNSLQOPEGIDRAKTSMLILHAADISHPAKTWKLHRTWMTALMEEFFRQ 394  
  
QY 379 ERELGLPFPCLDRTSTLVAQSOIGFDIFVEPTFSLTDAEKSQVPLADEDSKSNQ- 437  
DB 395 ERELGLPFPCLDRKSTWVAQSOIGFDIFVEPTFSLTDAEKSQVPLADEDSKSNQ- 454  
  
QY 438 -----PSFQWRQPSLDVEVGDPN-----DVSFRSTWVKRQENKQ 475  
DB 455 YGASSTWIGFHVADSLRSTNKGSCVCGSVAPDYSLSAVDLKSKFNVLVDIQQNKR 514  
  
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AC Q9EPR9;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Phosphodiesterase 1A.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wistar; TISSUE=Brain;

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RA Prime G.R., Sutor B.;
RT "Phosphodiesterase 1A (PDE1A) in rat brain.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF327838; AAG48736.1;
DR EMBL: AB038213; BAB20057.1; JOINED.
DR EMBL: AB038214; BAB20057.1; JOINED.
DR EMBL: AB038215; BAB20057.1; JOINED.
DR EMBL: AB038216; BAB20057.1; JOINED.
DR EMBL: AB038217; BAB20057.1; JOINED.
DR EMBL: AB038218; BAB20057.1; JOINED.
DR EMBL: AB038219; BAB20057.1; JOINED.
DR EMBL: AB038220; BAB20057.1; JOINED.
DR EMBL: AB038221; BAB20057.1; JOINED.
DR EMBL: AB038222; BAB20057.1; JOINED.
DR InterPro: IPR003607; Met_phosphohydro.
DR InterPro: IPR002073; PDEase.
DR Pfam: PF00233; PDEase; 1.
DR SMART: SM00471; HGC; 1.
DR PROSITE: PS00126; PDEASE_I; 1.
SQ SEQUENCE 542 AA; 61863 MW; 8793A7A0A58976F4 CRC64;

Query Match 58.0%; Score 1551.5; DB 11; Length 542;
Best Local Similarity 60.5%; Pred. No. 5.2e-116;
Matches 297; Conservative 84; Mismatches 81; Indels 29; Gaps 3;

QY 19 LRYVMKQLENGEINIEELKKNLEYTASLEAVYIDETROILDTDELOELRSDAVPSEVR 78
DB 35 LRLCVKQLEKGDVNVYDLKKNIEYAAVLEAVYIDETRLRLDTDELSDIQDVPSEVR 94
QY 79 DNLASTFTQOARAKRAAEKPKFRSIVHAVAQGIFFVERMFRRTYTSVGPTYSTAVLNCL 138
DB 95 DNLASTFTTRKMGTKKKPEKPKFRSIVHAVAQGIFFVERMYRKNYHMGVLTYPAAVIVTL 154
QY 139 KNLDLWCDFVSLNQAADHALRTIVFELLTRHNLISRKIPTVFLMSFLDALETGYGKY 198
DB 155 KEYDKMSFDFVFNALNEASGSHSKFMIYELFTSNDLINRKFIPVSCLIAPFAEALEVGYSKH 214
QY 199 KNPYHNQIHAADVDTQVHCHLRTGMVHCLSEIELLAIFFAAAIHDYEHGTGTFNFIQT 258
DB 215 KNPYHNLVHAADVDTQVHYIMLHTGIMHMLTELEILAMVFAAAVHDYEHGTGTFNFIQT 274
QY 259 KSCAIVYNDRSVLENHHTSSVFLRMQDDEMIENLTKEDEFVELRALVIEVMTATDMSK 318
DB 275 RSDVALYVNDRSVLENHHTSSVFLRMQDDEMIENLTKEDEFVELRALVIEVMTATDMSK 334
QY 319 HFQOVTMTALQQLERIDKPKALSLLHAADISHTPKOWLVHSRWTKALMEERFROGDK 378
DB 335 HFQOIKNRSSLOQPGIDRAKTSMLLHAADISHPAKTWKLVHRTWALMEERFLOGDK 394
QY 379 EALGLPFPPLCDRTSLTVAQSGIIGFIDFIVPTPTSTLTVDAEKSVOPLADEDSKNOP 438
DB 395 EALGLPFPPLCDRKTSTVAQSGIIGFIDFIVPTPTSTLTVDAEKSVOPLADEDSKNOP 451
QY 439 SFQWRQPSLDVEG-----DPN-----PDVVSFRSTWVKRIQEN 472
DB 452 SSNGYASSSTWIGFHVADALRSNTKCMDSGTAPDYSLSAVDLKSFKNLVDIIQON 511
QY 473 KOKWKERAASG 483
DB 512 KKKWELAAQG 522

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Q9COK8 PRELIMINARY; PRT: 511 AA.
AC Q9COK8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Calmodulin-dependent phosphodiesterase.
GN HSPDE1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21240211; PubMed=11342109;
RA Michibata H., Yanaka N., Kanoh Y., Okumura K., Omori K.;
RT "Human Ca2+/calmodulin-dependent phosphodiesterase PDE1A: novel splice
RT variants, their specific expression, genomic organization, and
RT chromosomal localization.";
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Job time : 74 secs

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Job time : 74 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 16:44:00 ; Search time 10905:Seconds  
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Title: US-09-663-481-2  
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Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

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- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
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- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	3091	100.0	3091	6	AXI39124 Sequence
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3	2317	94.4	3236	9	BC032226 Homo sapi
4	2700.8	87.4	3512	9	AB060237 Macaca fa
5	2407	77.9	2652	9	U86078 Homo sapien
6	2110	68.3	2265	9	U56976 Human calmo
7	1589.2	51.4	2986	10	L01695 Mus musculu
8	1383.4	44.8	180971	9	AC079310 Homo sapi
9	1348.2	43.6	195516	2	AC053540 Homo sapi
10	1347.6	43.6	1844	6	AR016548 Sequence
11	1347.6	43.6	1844	6	AR021268 Sequence
12	1347.6	43.6	1844	6	AR036822 Sequence
13	1347.6	43.6	1844	6	I30438 Sequence 26
14	1347.6	43.6	1844	6	I35682 Sequence 26
15	1341.8	43.4	1842	4	M94867 Bovine 63 k
16	1335.2	43.2	1831	10	M94537 Rattus norv
17	1327.2	42.9	1806	10	AF327906 Rattus no
18	601.2	19.5	2831	9	AK094180 Homo sapi
19	600	19.4	3209	9	AK091734 Homo sapi
20	599.6	19.4	2087	10	L76947 Mus musculu
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23	599.6	19.4	6154	10	BC032277 Mus muscu
24	598	19.3	2693	6	AR016560 Sequence
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35	593.6	19.2	3187	10	U56649 Mus musculu
36	593	19.2	1808	10	AF327838 Rattus no
37	590.4	19.1	1778	4	AF252536 Canis fam
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ALIGNMENTS

RESULT 1  
AXI39124  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AXI39124  
Sequence 2 from Patent EP1085092.  
AXI39124  
AXI39124.1 GI:14274800  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
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Fidock,M.D.  
Phosphodiesterase enzymes  
Patent: EP 1085092-A 2 21-MAR-2001;

AXI39124  
Sequence 2 from Patent EP1085092.  
AXI39124  
AXI39124.1 GI:14274800  
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Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
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Fidock,M.D.  
Phosphodiesterase enzymes  
Patent: EP 1085092-A 2 21-MAR-2001;

AXI39124  
Sequence 2 from Patent EP1085092.  
AXI39124  
AXI39124.1 GI:14274800  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
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Fidock,M.D.  
Phosphodiesterase enzymes  
Patent: EP 1085092-A 2 21-MAR-2001;



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RESULT 2  
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LOCUS  
DEFINITION Homo sapiens mRNA for 3'5' cyclic nucleotide phosphodiesterase 1B2 (PDE1B2 gene).  
ACCESSION AJ401609  
VERSION AJ401609.1 GI:16151612  
KEYWORDS 3'5' cyclic nucleotide phosphodiesterase 1B2; alternative splicing; PDE1B2 gene.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 Fidock, M., Miller, M. and Lanfear, J.  
AUTHORS Isolation and differential tissue distribution of two human cDNAs  
TITLE encoding PDE1 splice variants  
JOURNAL Cell. Signal. 14 (1), 53-60 (2002)  
MEDLINE 21614508  
PUBMED 11747989  
REFERENCE 2 (bases 1 to 2985)  
AUTHORS Fidock, M.D.  
TITLE Direct Submission  
JOURNAL Submitted (18-AUG-2000) Fidock M.D., Discovery Biology, Pfizer  
Global Research and Development, Ransgate Road, Sandwich, Kent CT13 9NU, UNITED KINGDOM  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2969; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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[illegible]

RESULT 3	
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LOCUS	3236 bp mRNA linear PRI 26-JUN-2002
DEFINITION	Homo sapiens, phosphodiesterase 1B, calmodulin-dependent, clone
	MG:34576 IMAGE:5200139, mRNA, complete cds.
ACCESSION	BC032226
VERSION	BC032226.1 GI:21594889
KEYWORDS	MGC.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 3236)
JOURNAL	Strausberg, R.
	Direct Submission
	Submitted (06-JUN-2002) National Institutes of Health, Mammalian
	Gene Collection (MGC), Cancer Genomics Office, National Cancer
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
	USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk
	Email: <a href="mailto:cgaphs-r@mail.nih.gov">cgaphs-r@mail.nih.gov</a>
	Tissue Procurement: Life Technologies, Inc.
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: National Institutes of Health Intramural
	Sequencing Center (NISC),
	Gaithersburg, Maryland;
	Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>

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ACCESSION AB060237
VERSION AB060237.1 GI:13676491
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Macaca fascicularis (crab-eating macaque)
ORGANISM Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
REFERENCE 1 (sites)
Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
libraries
Unpublished
2 (bases 1 to 3512)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (17-APR-2001) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)
Lab host: TOP10
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: DraIII (CACTGTGTC)
R. Site2: DraIII (CACCATGTC)
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGTCGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
the DraIII sites can be used to isolate the cDNA insert. Libraries
were constructed by oligo-capping method
(Sugano et al., , Institute of Medical Science, University of
Tokyo).
Custom primer used for sequencing
( 5' end primer [CTTCTGCTCTAAAGCTGGC];
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LOCUS			
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AUTHORS	Yu, J., Frazier, A.L.B., Wolda, S.L., Florio, V.A., Martins, T.J., Snyder, P.B., Harris, E.A.S., McCaw, K.N., Farrell, C.A., Steiner, B., Bentley, J.K., Beavo, J.A., Ferguson, K. and Gellinas, R.		
TITLE	Identification and characterisation of a human calmodulin-stimulated phosphodiesterase PDE1B cell. Signal. 9 (7), 519-529 (1997)		
JOURNAL	98081132		
MEDLINE	PUBMED 9419816		
REFERENCE	2 (bases 1 to 2652)		
AUTHORS	Yu, J., Frazier, A.L.B. and Wolda, S.L.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-JAN-1997) Research, ICOS Corporation, 22021 20th Ave SE, Bothell, WA 98021, USA		
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VERSION U66976.1
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SOURCE Homo sapiens (human)
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ACCESSION L01695  
VERSION L01695.1 GI:200269



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VERSION  
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ORGANISM  
REFERENCE  
AUTHORS

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Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,  
Burkett, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carton, T.F.,  
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Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J.,  
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Karlovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C.,  
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,  
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Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R.,  
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http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L.,  
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Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D.,  
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Washington, C., Watlington, S., Williams, G., Williamson, A.,  
Wlezyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J.,  
Zorrilla, S., Zuchner, L., and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 180971)  
Worley, K.C.  
Direct Submission  
Submitted (27-AUG-2000) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 180971)  
Worley, K.C.  
Direct Submission  
Submitted (01-JAN-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
4 (bases 1 to 180971)  
Worley, K.C.  
Direct Submission  
Submitted (15-MAR-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
5 (bases 1 to 180971)  
Worley, K.C.  
Direct Submission  
Submitted (27-APR-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jan 11 2003 this sequence version replaced gi:11968205.  
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email  
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the  
entire insert of this clone. Overlapping regions of clones are only  
sequenced and submitted once, so the sequence for the remainder of  
the insert may be found in the record for the adjacent clones.  
Overlapping clones are noted at the beginning and end of the  
Features listing.

ANNOTATION OF FEATURES:  
STSs are identified using ePCR (Genome Res. 7:541-550) searches  
of a local database that includes entries from dbSTS, GDB, and  
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,  
unpublished.) for Human and Mouse sequences.  
Genes and Region of sequence similarity are identified by BLAST  
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the  
EST and cDNA sequences. Genes demonstrate at least two exons  
flanked by consensus splice sites that maintained sequence  
continuity across the splice junctions. Sequences that are not  
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum  
standard of double strand coverage with a minimum of 2 clones and 2  
reads with no ambiguities or 2 chemistries with a minimum of 2  
clones and 3 reads with no ambiguities. If the sequence quality for  
a region does not meet this standard, it will be indicated in the  
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality  
standards - estimated error rate less than 1 per 10,000 bases.  
Reports of lowest quality individual bases and measures of base  
quality are listed below. Description of the metrics can be found  
at URL:

QUALSTAT-REPORT-----			
Summary Statistics			
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Fraction of Phrap values less than 40 :	8.90355e-06		
Number of consensus changing edits:	50		
Number of N's in consensus :	0		
Consensus changing edits			
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5337	tgaagatat(n)catatataa	tgaagatat(t)catatataa	
5355	atataatat(n)ttttttgtt	atataatat(a)ttttttgtt	
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Distribution of Quality < 40 Bases

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Phrap Value Range

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AUTHORS  
TITLE  
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COMMENT

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SEQUENCE, 42 unordered pieces.  
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AC053540.2 GI:7677988  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 195516)  
Waterston, R.H.  
The sequence of Homo sapiens clone  
Unpublished  
2 (bases 1 to 195516)  
Waterston, R.H.  
Direct Submission  
Submitted (16-Apr-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
On May 2, 2000 this sequence version replaced gi:7577687.

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
----- Project Information -----  
Center project name: H\_NH0774014  
----- Summary Statistics -----







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DEFINITION Sequence 26 from patent US 5776752.  
ACCESSION AR016548  
VERSION AR016548.1 GI:3972825  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1844)  
AUTHORS Beavo,J.A., Bentley,J.Kelley., Charbonneau,H. and Sonnenburg,W.K.  
TITLE Isolated and purified calcium/calmodulin stimulated cyclic  
nucleotide phosphodiesterases  
JOURNAL Patent: US 5776752-A 26 07-JUL-1998;  
FEATURES Location/Qualifiers  
source 1. .1844  
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BASE COUNT 417 a 551 c 514 g 362 t



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DEFINITION Sequence 26 from patent US 5800987.
ACCESSION AR036822
VERSION AR036822.1 GI:5954678
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1844)
AUTHORS Beavo, J.A., Bentley, J.K., Charbonneau, H., and Sonnenburg, W.K.
TITLE Assay methods using DNA encoding mammalian phosphodiesterases
JOURNAL Patent: US 5800987-A 26 01-SEP-1998;
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Query Match 43.6%; Score 1347.6; DB 6; Length 1844;
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QY 475 GTTCGGGAGAACATACACCTCTGTGGGCCCCACCTTACTTACTTGTGGGTCTCAACTGTCT 534
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DB	521	GTTCCGGAGAACATACACCTCTGTGGGCCCAACTTACTCTACTGCGGTTCTCAACTGTCT	580
QY	535	CAAGAACTGGATCTCTGGTGCTTTGATGTCTTTTCCCTTGAACCAAGCAGCAGATGACCA	594
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QY	835	TGCTGCAGCTATCCATGATTATGAGCACACGGGCACATACCAACAGCTTCCACATCCAGAC	894
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DB	941	CAAAATCGAATGCGCCATCTGTACACGACCCGCTCAGTCTGGAGAATCACCACATCAG	1000
QY	955	CTCTGTTTTCCGATTTGATGAGGATGATGAGATCAACATTTTCATCAACCTCACCAGGA	1014
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DEFINITION Sequence 26 from patent US 5580771.				
ACCESSION I30438				
VERSION I30438.1 GI:1821229				
KEYWORDS Unknown.				
SOURCE Unknown.				
ORGANISM Unclassified.				
REFERENCE 1 (bases 1 to 1844)				
AUTHORS Baavo,J.A., Charbonneau,H. and Sonnenburg,W.K.				
TITLE DNA encoding Phosphodiesterases.				
JOURNAL Patent: US 5580771-A 26 03-DEC-1996;				
FEATURES location/Qualifiers				
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BASE COUNT 417 a 551 c 362 t				
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Db	284	AAACCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTCTATATAGATGAGACTCGGCAAT		343
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Db	404	GGACTGGCTGGCTCCACCTTCACCCAGCAGACCCCGGGCCAAAGGCCCGAG---CGAAGA		460
Qy	415	GAAGCCCAAGTTCGGAAGCAATTGTGACGCTGTGCAAGGCTGGGATCTCTCGTGAACCGAT		474
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Db	1838	CCGAAG	1843
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ACCESSION I35682			
VERSION I35682.1 GI:2087533			
KEYWORDS			
SOURCE Unknown.			
ORGANISM Unknown.			
REFERENCE Unclassified.			
AUTHORS 1 (bases 1 to 1844)			
Beavo,J.A., Bentley,K.J., Charbonneau,H. and Sonnenburg,W.K.			
TITLE DNA encoding mammalian phosphodiesterases			
JOURNAL Patent: US 5602019-A 26 11-FEB-1997;			
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QY	535	CAAGAACTGGATCTCTGGTGTCTTTGATGCTTTTTCTCTGAACCAGGACGACATGACCA	594
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Db 1720 --GGGGCTGGCCAGGCTCTCACTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1777  
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RESULT 15  
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LOCUS  
DEFINITION  
Bovine 63 kDa calmodulin-stimulated phosphodiesterase mRNA,  
complete cds.  
ACCESSION  
M94867.1 GI:162782  
VERSION  
63 kDa calmodulin-stimulated phosphodiesterase.  
KEYWORDS  
Bos taurus (cow)  
SOURCE  
ORGANISM  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 1842)  
REFERENCE  
AUTHORS  
Bentley, J.K., Kadlcek, A., Sherbert, C.H., Seger, D., and Beavo, J.A.  
TITLE  
Molecular cloning of cDNA encoding a '63'-kDa calmodulin-stimulated  
phosphodiesterase from bovine brain  
J. Biol. Chem. 267 (26), 18676-18682 (1992)  
92406781  
MEDLINE  
PUBMED  
1:26531  
REFERENCE  
2 (bases 1 to 1842)  
Direct Submission  
Beavo, J.A.  
TITLE  
Submitted (20-JUL-1992) Joe A. Beavo, Department of Pharmacology,  
SU-30, University of Washington, Seattle, WA 98195, USA  
JOURNAL  
COMMENT  
Original location text: Bos taurus cDNA to mRNA.  
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Location/Qualifiers  
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DELSPCBEAPAPAEDEHNQNGND"

BASE COUNT 417 a 552 c 511 g 362 t  
ORIGIN

Query Match 43.48; Score 1341.8; DB 4; Length 1842;  
Best Local Similarity 90.48; Pred. No. 0;  
Matches 1469; Conservative 0; Mismatches 147; Indels 9; Gaps 3;  
QY 175 GTCGCGTACATGCTGAAGCAGTGTGGAGATGGGAGATAAACATTCAGGAGCTGAAGAA 234  
Db 224 GCTCGCTACATGCTGAAGCAGTGTGGAGACGGGAGGTAAACATTCAGGAGCTGAAGAA 283  
QY 235 AAATCTGGAGTACAGCTTCTCTGCTGGAGCGCTGCTACATAGATGAGACACGGCAAT 294

Db	284	AAACCTCGAGTACACACGCTTCTCTGCTGGAGCGGCTATATAGATGAGACTCGGCAAAAT	343	
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Db	344	CCTGGACACGGAGGATGAGCTGCAGGAGCTGCGTCTGATGCGGTGCGCTTCAGAGGTGCG	403	
QY	355	GGACTGCTGGCCTCCACCTTCACCCAGCAGCGCGCGGCGCCAAAGCGCGCGAGCAGGA	414	
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QY	715	CAGAATCTTTACCAACACAGATCCACGACGCGGATGTTTACCACACAGCTCCATGCTTT	774	

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Job time : 10916 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 16:42:40 ; Search time 764 Seconds  
(without alignments)  
10921.417 Million cell updates/sec

Title: US-09-663-481-2  
Perfect score: 3091  
Sequence: 1 gtgaccacgcgtccggga.....aaaaaaaaaaaaaaaaaaaaa 3091

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3091	100.0	3091	22	AAFG2301 Human cyclic nucle
2	2903.6	93.9	3054	22	AAH57561 Human brain cell s
3	2106.8	68.2	2265	20	AAH26288 Human RPMI 8392 ce
4	1347.6	43.6	1844	16	AAQ83969 Cyclic-GMP stimula
5	1347.6	43.6	1844	18	AAAT67200 Bovine brain 63 kd
6	1347.6	43.6	1844	18	AAAT51105 cDNA for 63 kd cal
7	1347.6	43.6	1844	19	AAV48196 Bovine brain Ca2+/
8	1347.6	43.6	1844	19	AAV54753 63 kDa Cam-PDE DNA

9	1347.6	43.6	1844	19	AAV36148 Bovine Cam-PDE CDN
10	1347.6	43.6	1844	21	AAZ90372 Bovine brain 63 kd
11	1347.6	43.6	1844	25	ABX78849 Bovine brain cDNA
12	1342.8	43.4	1844	13	AAQ30175 63 kd Cam PDE cDNA
13	598	19.3	2693	16	AAQ83981 Cyclic-GMP stimula
14	598	19.3	2693	18	AAAT67202 Human brain 61 kDa
15	598	19.3	2693	18	AAAT51116 Hippocampus calcicu
16	598	19.3	2693	19	AAV54765 Human 61 kDa Cam-P
17	598	19.3	2693	19	AAV48208 Human Ca2+/calmodu
18	598	19.3	2693	19	AAV36160 cDNA encoding a hu
19	598	19.3	2693	21	AAZ90384 Human 61 kd Cam-PD
20	598	19.3	2693	25	ABX78861 Human cDNA encodin
21	593.2	19.2	2693	13	AAQ30187 cDNA insert of pca
22	579.8	18.8	2656	13	AAQ30172 Bovine lung 59 kd
23	579.8	18.8	2656	16	AAQ83964 Cyclic-GMP stimula
24	579.8	18.8	2656	18	AAAT67199 Bovine lung 59 kDa
25	579.8	18.8	2656	18	AAAT51091 Coding sequence fo
26	579.8	18.8	2656	19	AAV48191 Bovine lung Ca2+/c
27	579.8	18.8	2656	19	AAV54748 59 kDa Cam-PDE DNA
28	579.8	18.8	2656	19	AAV36143 Bovine Cam-PDE CDN
29	579.8	18.8	2656	21	AAZ90367 Bovine lung 59 kd
30	579.8	18.8	2656	25	ABX78844 Bovine heart cDNA
31	578.8	18.7	1625	16	AAQ83980 Cyclic-GMP stimula
32	578.8	18.7	1625	18	AAAT67201 Human brain 61 kDa
33	578.8	18.7	1625	18	AAAT51115 Hippocampus calcicu
34	578.8	18.7	1625	19	AAV54764 Human 61 kDa Cam-P
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36	578.8	18.7	1625	19	AAV36159 cDNA encoding a hu
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38	578.8	18.7	1625	25	ABX78860 Human cDNA encodin
39	578.8	18.7	2008	22	AAAD14515 Human phosphodiester
40	578.8	18.7	2008	22	AAAD14525 Human phosphodiester
41	578.8	18.7	2008	22	AAAF84074 Human 3', 5' cycli
42	578.8	18.7	2008	22	AAAF84084 Human 3', 5' cycli
43	577.2	18.7	1763	23	AAAT5915 cDNA encoding novel
44	574	18.6	1625	13	AAQ30186 cDNA insert of pHC
45	559.6	18.1	2291	16	AAQ83957 Cyclic-GMP stimula

## ALIGNMENTS

RESULT 1  
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ID AAF62301 standard; cDNA; 3091 BP.  
XX  
AC AAF62301;  
DT  
DT 06-JUN-2001 (first entry)  
XX  
DE Human cyclic nucleic acid phosphodiesterase PDE1B2 coding sequence.  
XX  
KW Human; cyclic nucleic acid phosphodiesterase; PDE1B2; sexual dysfunction;  
KW cardiovascular disease; gastrointestinal disorder; spleen; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 122..1672  
FT /tag= a  
FT /product= "PDE1B2"  
XX  
PN EP1085092-A1.  
XX  
PD 21-MAR-2001.  
XX  
PF 14-SEP-2000; 2000EP-0307982.  
PR 17-SEP-1999; 99GB-0022125.  
XX (PFIZ ) PFIZER LTD.  
PA (PFIZ ) PFIZER INC.  
XX



QY 1801 AAATGCCAGAGATTGGGGTTGGGAAAGGGCCCCCTCCCTGACACCCACTGGGGTG 1860  
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## RESULT 2

AAH57561

ID AAH57561 standard; cDNA; 3054 BP.

XX AAH57561;

AC AC

XX XX

DT 10-SEP-2001 (first entry)

XX Human brain cell specific cDNA sequence SEQ ID NO:401.

DE Human; tissue specific; diagnosis; brain; heart; skeletal muscle;

KW lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;

KW metabolic disease; developmental disease; cytostatic; immunomodulatory;

KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

XX Homo sapiens.

XX WO200132927-A2.

XX 10-MAY-2001.

XX 02-NOV-2000; 2000WO-US30396.

XX 04-NOV-1999; 99US-0163508.

XX (INCY-) INCYTE GENOMICS INC.

PI Sornasse T, Seilhamer JJ, Watson GA;

PI WPI, 2001-291057/30.

XX New cell and tissue specific polynucleotides useful for diagnosis,

XX prognosis or monitoring of treatments for disorders where the gene is

XX associated with a cancer, immunopathology or neuropathology -

PS Claim 1; Page 315; 327pp; English.

XX AAH57161 to AAH57576 represent cell and tissue specific polynucleotide

XX sequences (I). (I) can have cytostatic, immunomodulatory and

XX neuroprotective activities, and can be used in gene therapy. (I) and

XX proteins (II) encoded by then are used in high throughput screening

XX assays to select DNA molecules, RNA molecules, peptide nucleic acids,

XX mimetics, peptides, proteins, agonists, antagonists, antibodies or

XX their fragments, immunoglobulins, inhibitors, drug compounds and

XX pharmaceutical agents. Expression of (I) in a sample indicates the

XX differentiation of embryonic stem cells into a tissue selected from

XX brain, heart, kidney, liver, lung, skeletal muscle or pancreatic

XX tissues. (I) and (II) are used to produce an expression profile that

XX defines a metabolic or developmental process, treatment, condition,

XX disease or disorder. The gene profile can be used for diagnosis,

XX prognosis or monitoring of treatments and for investigating a

XX predisposition to a disorder where the gene is associated with a

XX cancer, immunopathology or neuropathology.

SQ Sequence 3054 BP; 671 A; 884 C; 830 G; 669 T; 0 other;

XX Query Match 93.9%; Score 2903.6; DB 22; Length 3054;

Best Local Similarity 99.9%; Pred. No. 0;				Matches 2906; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
QY	Db	175	GCTGGCTACATGGTGAAGCAGTGGAGAATGGGAGATTAACATTTGAGGAGCTGAAGAA	234			
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	Db	385 <td>GAAGCCCAAGTTCGGAAGCATTTGACAGCTGTGAGCGTGGGATCTTGGTGAAGCGAT<th>444</th><td></td><td></td><td></td></td>	GAAGCCCAAGTTCGGAAGCATTTGACAGCTGTGAGCGTGGGATCTTGGTGAAGCGAT <th>444</th> <td></td> <td></td> <td></td>	444			
	QY	475 <td>GTTCGGGAGAACATACACCTCTGTGGCGCCCACTTACTCTACTGTGCGTCTCAACTGTCT<th>534</th><td></td><td></td><td></td></td>	GTTCGGGAGAACATACACCTCTGTGGCGCCCACTTACTCTACTGTGCGTCTCAACTGTCT <th>534</th> <td></td> <td></td> <td></td>	534			
	Db	445 <td>GTTCGGGAGAACATACACCTCTGTGGCGCCCACTTACTCTACTGTGCGTCTCAACTGTCT<th>504</th><td></td><td></td><td></td></td>	GTTCGGGAGAACATACACCTCTGTGGCGCCCACTTACTCTACTGTGCGTCTCAACTGTCT <th>504</th> <td></td> <td></td> <td></td>	504			
	QY	535 <td>CAAGAACCTGGATCTGGTGTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT<th>594</th><td></td><td></td><td></td></td>	CAAGAACCTGGATCTGGTGTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT <th>594</th> <td></td> <td></td> <td></td>	594			
	Db	505 <td>CAAGAACCTGGATCTGGTGTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT<th>564</th><td></td><td></td><td></td></td>	CAAGAACCTGGATCTGGTGTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT <th>564</th> <td></td> <td></td> <td></td>	564			
	QY	595 <td>TGCGCTGAGCAATGTTTTCAGTGTGCTGAGTTCGCGATTAACCTCATCAGCGCTTCAA<th>654</th><td></td><td></td><td></td></td>	TGCGCTGAGCAATGTTTTCAGTGTGCTGAGTTCGCGATTAACCTCATCAGCGCTTCAA <th>654</th> <td></td> <td></td> <td></td>	654			
	Db	565 <td>TGCGCTGAGCAATGTTTTCAGTGTGCTGAGTTCGCGATTAACCTCATCAGCGCTTCAA<th>624</th><td></td><td></td><td></td></td>	TGCGCTGAGCAATGTTTTCAGTGTGCTGAGTTCGCGATTAACCTCATCAGCGCTTCAA <th>624</th> <td></td> <td></td> <td></td>	624			
	QY	655 <td>GATTCGCCACTGTGTTTGTGATGATTTCTGAGTTCGCTGAGTTCGAGACAGGCTATGGGA<th>714</th><td></td><td></td><td></td></td>	GATTCGCCACTGTGTTTGTGATGATTTCTGAGTTCGCTGAGTTCGAGACAGGCTATGGGA <th>714</th> <td></td> <td></td> <td></td>	714			
	Db	625 <td>GATTCGCCACTGTGTTTGTGATGATTTCTGAGTTCGCTGAGTTCGAGACAGGCTATGGGA<th>684</th><td></td><td></td><td></td></td>	GATTCGCCACTGTGTTTGTGATGATTTCTGAGTTCGCTGAGTTCGAGACAGGCTATGGGA <th>684</th> <td></td> <td></td> <td></td>	684			
	QY	715 <td>CAAGAACTCTTACACAACACAGATCCACGACGAGCTGTTTACCGACAGCTTCCATTCCTT<th>774</th><td></td><td></td><td></td></td>	CAAGAACTCTTACACAACACAGATCCACGACGAGCTGTTTACCGACAGCTTCCATTCCTT <th>774</th> <td></td> <td></td> <td></td>	774			
	Db	685 <td>CAAGAACTCTTACACAACACAGATCCACGACGCGATGTTTACCGACAGCTTCCATTCCTT<th>744</th><td></td><td></td><td></td></td>	CAAGAACTCTTACACAACACAGATCCACGACGCGATGTTTACCGACAGCTTCCATTCCTT <th>744</th> <td></td> <td></td> <td></td>	744			
	QY	775 <td>CTTGTCTCCGACAGGAGTGTGCACTGCCTGTCCGAGATTTGAGTCTCTGCGCATTCATTC<th>834</th><td></td><td></td><td></td></td>	CTTGTCTCCGACAGGAGTGTGCACTGCCTGTCCGAGATTTGAGTCTCTGCGCATTCATTC <th>834</th> <td></td> <td></td> <td></td>	834			
	Db	745 <td>CTTGTCTCCGACAGGAGTGTGCACTGCCTGTCTCGAGATTTGAGTCTCTGCGCATTCAT<th>804</th><td></td><td></td><td></td></td>	CTTGTCTCCGACAGGAGTGTGCACTGCCTGTCTCGAGATTTGAGTCTCTGCGCATTCAT <th>804</th> <td></td> <td></td> <td></td>	804			
	QY	835 <td>TGCTGCAGCTATCCATGATATGAGCACAGCGGCACTACCAACAGCTTCCACATCCAGAC<th>894</th><td></td><td></td><td></td></td>	TGCTGCAGCTATCCATGATATGAGCACAGCGGCACTACCAACAGCTTCCACATCCAGAC <th>894</th> <td></td> <td></td> <td></td>	894			
	Db	805 <td>TGCTGCAGCTATCCATGATATGAGCACAGCGGCACTACCAACAGCTTCCACATCCAGAC<th>864</th><td></td><td></td><td></td></td>	TGCTGCAGCTATCCATGATATGAGCACAGCGGCACTACCAACAGCTTCCACATCCAGAC <th>864</th> <td></td> <td></td> <td></td>	864			
	QY	895 <td>CAAGTCAGAAATGTGCCATCGTGTACAATGATGCTGAGTGTGAGATCCACACATCAG<th>954</th><td></td><td></td><td></td></td>	CAAGTCAGAAATGTGCCATCGTGTACAATGATGCTGAGTGTGAGATCCACACATCAG <th>954</th> <td></td> <td></td> <td></td>	954			
	Db	865 <td>CAAGTCAGAAATGTGCCATCGTGTACAATGATGCTGAGTGTGAGATCCACACATCAG<th>924</th><td></td><td></td><td></td></td>	CAAGTCAGAAATGTGCCATCGTGTACAATGATGCTGAGTGTGAGATCCACACATCAG <th>924</th> <td></td> <td></td> <td></td>	924			
	QY	955 <td>CTCTGTTTCCGATTGATGAGGATGATGAGATGAACATTTTCAATCAACCTCAGCAAGGA<th>1014</th><td></td><td></td><td></td></td>	CTCTGTTTCCGATTGATGAGGATGATGAGATGAACATTTTCAATCAACCTCAGCAAGGA <th>1014</th> <td></td> <td></td> <td></td>	1014			
	Db	925 <td>CTCTGTTTCCGATTGATGAGGATGATGAGATGAACATTTTCAATCAACCTCAGCAAGGA<th>984</th><td></td><td></td><td></td></td>	CTCTGTTTCCGATTGATGAGGATGATGAGATGAACATTTTCAATCAACCTCAGCAAGGA <th>984</th> <td></td> <td></td> <td></td>	984			
	QY	1015 <td>TGAGTTTGTAGAACTCCGAGCCCTGGTCAATTTGAGATGTTGTGGCCAGACATGCTCTG<th>1074</th><td></td><td></td><td></td></td>	TGAGTTTGTAGAACTCCGAGCCCTGGTCAATTTGAGATGTTGTGGCCAGACATGCTCTG <th>1074</th> <td></td> <td></td> <td></td>	1074			
	Db	985 <td>TGAGTTTGTAGAACTCCGAGCCCTGGTCAATTTGAGATGTTGTGGCCAGACATGCTCTG<th>1044</th><td></td><td></td><td></td></td>	TGAGTTTGTAGAACTCCGAGCCCTGGTCAATTTGAGATGTTGTGGCCAGACATGCTCTG <th>1044</th> <td></td> <td></td> <td></td>	1044			
	QY	1075 <td>CCATTTCCAGCAAGTGAAGACCATGAAGACAGCTTTCAGACAGCTGGAGAGATTCACAA<th>1134</th><td></td><td></td><td></td></td>	CCATTTCCAGCAAGTGAAGACCATGAAGACAGCTTTCAGACAGCTGGAGAGATTCACAA <th>1134</th> <td></td> <td></td> <td></td>	1134			
	Db	1045 <td>CCATTTCCAGCAAGTGAAGACCATGAAGACAGCTTTCAGACAGCTGGAGAGATTCACAA<th>1104</th><td></td><td></td><td></td></td>	CCATTTCCAGCAAGTGAAGACCATGAAGACAGCTTTCAGACAGCTGGAGAGATTCACAA <th>1104</th> <td></td> <td></td> <td></td>	1104			
	QY	1135 <td>GCCCAAGGCCCTGTCTCTACTGCTCCATGCTGAGATGAGTCCGACACCAACAGCAGTG<th>1194</th><td></td><td></td><td></td></td>	GCCCAAGGCCCTGTCTCTACTGCTCCATGCTGAGATGAGTCCGACACCAACAGCAGTG <th>1194</th> <td></td> <td></td> <td></td>	1194			
	Db	1105 <td>GCCCAAGGCCCTGTCTCTACTGCTCCATGCTGAGATGAGTCCGACACCAACAGCAGTG<th>1164</th><td></td><td></td><td></td></td>	GCCCAAGGCCCTGTCTCTACTGCTCCATGCTGAGATGAGTCCGACACCAACAGCAGTG <th>1164</th> <td></td> <td></td> <td></td>	1164			
	QY	1195 <td>GTTGGTCCACAGCGCTTGACCAAGGCCCTCATGGAGAAATTTCTTCCTCAGGTTGACAA<th>1254</th><td></td><td></td><td></td></td>	GTTGGTCCACAGCGCTTGACCAAGGCCCTCATGGAGAAATTTCTTCCTCAGGTTGACAA <th>1254</th> <td></td> <td></td> <td></td>	1254			
	Db						
	Db	1165	(TTTGTCTCACAGCCGTTGGACCAAGGCCCTCATGGAGAAATTTCTTCGTCAGGTTGACAA <th>1214</th> <td></td> <td></td> <td></td>	1214			
	QY	1255	(GAGGCAGAGTTGGCCCTGGCCCTTTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGGC <th>1314</th> <td></td> <td></td> <td></td>	1314			
	Db	1225	(GAGGCAGAGTTGGCCCTGGCCCTTTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGGC <th>1284</th> <td></td> <td></td> <td></td>	1284			
	QY	1315	(ACAGTCTCAGATAGAGTTTCATCGACTTCAATTTGTGGAGCCACATTCCTGTGTGCTGACTGA <th>1374</th> <td></td> <td></td> <td></td>	1374			
	Db	1285	(ACAGTCTCAGATAGAGTTTCATCGACTTCAATTTGTGGAGCCACATTCCTGTGTGCTGACTGA <th>1344</th> <td></td> <td></td> <td></td>	1344			
	QY	1375	(CTGGCAGAGAAAGAGTGTTCAGCCCCCTGGCGGATGAGGACTTCCAAAGTCTTAAACACAGCC <th>1434</th> <td></td> <td></td> <td></td>	1434			
	Db	1345	(CTGGCAGAGAAAGAGTGTTCAGCCCCCTGGCGGATGAGGACTTCCAAAGTCTTAAACACAGCC <th>1404</th> <td></td> <td></td> <td></td>	1404			
	QY	1435	(AGCTTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGGAGACCCCAACCTGTATGT <th>1494</th> <td></td> <td></td> <td></td>	1494			
	Db	1405	(AGCTTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGGAGACCCCAACCTGTATGT <th>1464</th> <td></td> <td></td> <td></td>	1464			
	QY	1495	(GTGAGCTTTCGTTTCCACTGGGTCAAGCGCATTCAGGCAATTAAGCAAGATTCGAAGGA <th>1554</th> <td></td> <td></td> <td></td>	1554			
	Db	1465	(GTGAGCTTTCGTTTCCACTGGGTCAAGCGCATTCAGGCAATTAAGCAAGATTCGAAGGA <th>1524</th> <td></td> <td></td> <td></td>	1524			
	QY	1555	(ACGGGCAAGTGGGATCACCAACAGATGTCCATTGACAGAGTTCGCCCTGTGAAGA <th>1614</th> <td></td> <td></td> <td></td>	1614			
	Db	1525	(ACGGGCAAGTGGGATCACCAACAGATGTCCATTGACAGAGTTCGCCCTGTGAAGA <th>1584</th> <td></td> <td></td> <td></td>	1584			
	QY	1615	(AGAGGCCCCCCCATCCCTGGCGAAGATGAACACACAGATGGGAATCTGGATTAGCC <th>1674</th> <td></td> <td></td> <td></td>	1674			
	Db	1585	(AGAGGCCCCCCCATCCCTGGCGAAGATGAACACACAGATGGGAATCTGGATTAGCC <th>1644</th> <td></td> <td></td> <td></td>	1644			
	QY	1675	(CTGGGCTGGCCAGGCTTCATTTGAGTCCAAAGTGTGATGTCTCATCAGCACCATTCCAT <th>1734</th> <td></td> <td></td> <td></td>	1734			
	Db	1645	(CTGGGCTGGCCAGGCTTCATTTGAGTCCAAAGTGTGATGTCTCATCAGCACCATTCCAT <th>1704</th> <td></td> <td></td> <td></td>	1704			
	QY	1735	(CAGGACTGCTGCCCATCTGCTCCAAAGGAGCGTGTGCTGGAAGAAACACACCCACTG <th>1794</th> <td></td> <td></td> <td></td>	1794			
	Db	1705	(CAGGACTGCTGCCCATCTGCTCCAAAGGAGCGTGTGCTGGAAGAAACACACCCACTG <th>1764</th> <td></td> <td></td> <td></td>	1764			
	QY	1795	(AAGGCCAAATCCAGAGATTTGGGGTTGGGAAAGGCGCCCTCCACCTGACACCCACT <th>1854</th> <td></td> <td></td> <td></td>	1854			
	Db	1765	(AAGGCCAAATCCAGAGATTTGGGGTTGGGAAAGGCGCCCTCCACCTGACACCCACT <th>1824</th> <td></td> <td></td> <td></td>	1824			
	QY	1855	(GGGTGCACTTTAATGTTCCGGCAGCAAGACTTGGGAACTTCAGGCTCCAGTGTGCTACT <th>1914</th> <td></td> <td></td> <td></td>	1914			
	Db	1825	(GGGTGCACTTTAATGTTCCGGCAGCAAGACTTGGGAACTTCAGGCTCCAGTGTGCTACT <th>1884</th> <td></td> <td></td> <td></td>	1884			
	QY	1915	(GTGCCCATCCCTCAGCTCTGGATTTCTTTCATGGCCAGGTGCTGCCAGGAGCGGGA <th>1974</th> <td></td> <td></td> <td></td>	1974			
	Db	1885	(GTGCCCATCCCTCAGCTCTGGATTTCTTTCATGGCCAGGTGCTGCCAGGAGCGGGA <th>1944</th> <td></td> <td></td> <td></td>	1944			
	QY	1975	(GCTTCTGGAGGCTTCCAGGGCTTGGGAAAGGCTCAGAGATGCCAGCCCTGGGACC <th>2034</th> <td></td> <td></td> <td></td>	2034			
	Db	1945	(GCTTCTGGAGGCTTCCAGGGCTTGGGAAAGGCTCAGAGATGCCAGCCCTGGGACC <th>2004</th> <td></td> <td></td> <td></td>	2004			
	QY	2035	(TCCCCCATCTCTTTTGGCTCCAAAGTTTCTAAGCAATACATTTTGGGGGTTCCCTCAGCCC <th>2094</th> <td></td> <td></td> <td></td>	2094			
	Db	2005	(TCCCCCATCTCTTTTGGCTCCAAAGTTTCTAAGCAATACATTTTGGGGGTTCCCTCAGCCC <th>2064</th> <td></td> <td></td> <td></td>	2064			
	QY	2095	(CCACCCACAGATCTTAGCTGGCAGGTCTGGGTGCCCTTTTCTCCCTCCCTGGGAGGCTG <th>2154</th> <td></td> <td></td> <td></td>	2154			
	Db	2065	(CCACCCACAGATCTTAGCTGGCAGGTCTGGGTGCCCTTTTCTCCCTCCCTGGGAGGCTG <th>2124</th> <td></td> <td></td> <td></td>	2124			
	QY	2155	(GAATAGGATAGAAAGCTGGGGTTTTCAGAGCCCTATGTGTGGGGAGGGAGTGGATTC <th>2214</th> <td></td> <td></td> <td></td>	2214			
	Db	2125	(GAATAGGATAGAAAGCTGGGGTTTTCAGAGCCCTATGTGTGGGGAGGGAGTGGATTC <th>2184</th> <td></td> <td></td> <td></td>	2184			
	QY	2215	(TTCAGGGCATGGTACCTTTCTTAGGATCTGGGAATGGGGTGGAGGAGCATCTCTCTTCAAC <th>2274</th> <td></td> <td></td> <td></td>	2274			
	Db	2185	(TTCAGGGCATGGTACCTTTCTTAGGATCTGGGAATGGGGTGGAGGAGCATCTCTCTTCAAC <th>2244</th> <td></td> <td></td> <td></td>	2244			
	QY	2275	(CCAGAAATTCGCGTGTCTTTCAGCCCATCTCCAGCCCTGATCTCTGAAATCTCTCTCCCTC <th>2334</th> <td></td> <td></td> <td></td>	2334			
	Db	2245	(CCAGAAATTCGCGTGTCTTTCAGCCCATCTCCAGCCCTGATCTCTGAAATCTCTCTCCCTC <th>2304</th> <td></td> <td></td> <td></td>	2304			

QY 2335 CTTTCTGATACAGTGGGCAAAAGGAGCCATTGTGACACAGGGGCTGCGGAGGCT 2394  
 Db 2305 CTTTCTGATAGTGGGCAAAAGGAGCCATTGTGACACAGGGGCTGCGGAGGCT 2364  
 QY 2395 TTCTCGGACCTTCTTGGGACTGTGTGCGGCCCCGCGGCTTGTGCGCTGCCCTGAGTC 2454  
 Db 2365 TTCTCGGACCTTCTTGGGACTGTGTGCGGCCCCGCGGCTTGTGCGCTGCCCTGAGTC 2424  
 QY 2455 CGGAGCCCTTTGCGCTTCTTCTCCCTGGGCTGGGAGGCTCCATCGGACCAATGTCT 2514  
 Db 2425 CGGAGCCCTTTGCGCTTCTTCTCCCTGGGCTGGGAGGCTCCATCGGACCAATGTCT 2484  
 QY 2515 GTAAAGTCTTTGAGGATCTCCCAAGCAAAAGCACCCTTCAGATGTATCGACACCAAGCTGG 2574  
 Db 2485 GTAAAGTCTTTGAGGATCTCCCAAGCAAAAGCACCCTTCAGATGTATCGACACCAAGCTGG 2544  
 QY 2575 GTTAGGTCAGAGGTGCTTGGGAGGCTGAGTATCTGCTGATGTGTAAGAGAGAGGCTCT 2634  
 Db 2545 GTTAGGTCAGAGGTGCTTGGGAGGCTGAGTATCTGCTGATGTGTAAGAGAGAGGCTCT 2604  
 QY 2635 GTCCCTCTCTCCACGCTCCAGAACTGGCCAGCTGCAGGCACTAAGAGCTCTCTCC 2694  
 Db 2605 GTCCCTCTCTCCACGCTCCAGAACTGGCCAGCTGCAGGCACTAAGAGCTCTCTCC 2664  
 QY 2695 TGAGACAAGTGAAGGCTAGTCGGTGAAGAGGAGATGAGAGGGGCTCAGGGCTGCTGCC 2754  
 Db 2665 TGAGACAAGTGAAGGCTAGTCGGTGAAGAGGAGATGAGAGGGGCTCAGGGCTGCTGCC 2724  
 QY 2755 TTCTGTCTCTGGAGAGAACCCAGGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 2814  
 Db 2725 TTCTGTCTCTGGAGAGAACCCAGGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 2784  
 QY 2815 CTTTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2874  
 Db 2785 CTTTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2844  
 QY 2875 TGTAATACCAACCACTGATTTGTACAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2934  
 Db 2845 TGTAATACCAACCACTGATTTGTACAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2904  
 QY 2935 GTCTCTAGACCTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2994  
 Db 2905 GTCTCTAGACCTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2964  
 QY 2995 GCATGTAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3054  
 Db 2965 GCATGTAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3024  
 QY 3055 AGAAGGAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3084  
 Db 3025 AGAAGGAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3054

RESULT 3

ID AAX26288 standard; cdna; 2265 BP.  
 XX AC AAX26288;  
 XX DT 26-MAY-1999 (first entry)  
 XX DE Human RPMI 8392 cell phosphodiesterase, PDE1B1 encoding cdna.  
 XX KW Antisense oligodeoxynucleotide; phosphodiesterase; PDE1B1; enzyme; PDE;  
 KW cell death; apoptosis; cancer; Ca2+-calmodulin; lymphoblastoid; RNase H;  
 KW RPMI 8392; RNA degradation; cAMP; immunoproliferative disorder; breast;  
 KW immune dysfunction; acute lympholytic leukemia; prostate; human; ss.  
 XX OS Homo sapiens.  
 XX PN US5885834-A.

PD 23-MAR-1999.  
 XX 30-SEP-1997; 97US-0940332.  
 XX 30-SEP-1996; 96US-0027207.  
 PR 30-SEP-1997; 97US-0940332.  
 XX (EPST/) EPSTEIN P M.  
 XX Epstein PM;  
 XX WPI; 1999-228548/19.  
 DR P-PSDB; AAW95110.  
 XX Antisense oligodeoxynucleotides specific for mRNA encoding  
 PT phosphodiesterase PDE1B1 enzymes and method for using them to induce  
 PT apoptosis of cells - useful in the treatment of immunoproliferative  
 PT disorders and immune dysfunctions  
 XX PS Disclosure: Fig 8A-D; 35pp; English.  
 XX The invention relates to antisense oligodeoxynucleotides (AS-ODN) which  
 CC will bind to mRNA encoding phosphodiesterase PDE1B1 enzymes and their use  
 CC in inducing programmed cell death (apoptosis) in cancer cells. PDE1 is a  
 CC Ca2+-calmodulin dependent phosphodiesterase found in cytosolic extracts  
 CC of human lymphoblastoid cell line, RPMI 8392. The method in which  
 CC programmed cell death is induced in cancer cells comprises: (1)  
 CC identifying the phosphodiesterase enzyme PDE1B1 in a cell line containing  
 CC the cancer cells; (2) synthesizing an AS-ODN inhibitor which will bind to  
 CC mRNA encoding PDE1B1; and (3) applying the AS-ODN to the cell line to  
 CC inhibit the enzymatic activity of the PDE1B1 and induce apoptosis in the  
 CC cells. The AS-ODNs inhibit the expression of a protein by two mechanisms:  
 CC (i) by degradation of the RNA by the ubiquitous enzyme RNase H, which  
 CC selectively cleaves the RNA of DNA-RNA heteroduplexes; and (ii) the  
 CC arrest of translation initiation caused by AS-ODN hybridization to the 5'  
 CC un-translated region or the translation initiation site on the mRNA.  
 CC Inhibition of phosphodiesterase (PDE) enzyme expression results in  
 CC elevated levels of cAMP in the cells due to PDE1B1 being involved in the  
 CC metabolism of cAMP. The elevated cAMP levels result in apoptosis by  
 CC inhibition of DNA synthesis. The method and AS-ODN are useful in inducing  
 CC cAMP stimulated apoptosis and in the treatment of immunoproliferative  
 CC disorders and immune dysfunctions such as acute lympholytic leukemia,  
 CC breast and prostate cancer. The present sequence represents a cDNA  
 CC encoding a human RPMI 8392 cell PDE1B1.  
 XX SQ Sequence 2265 BP; 507 A; 628 C; 627 G; 500 T; 3 other;  
 Query Match 68.2%; Score 2106.8; DB 20; Length 2265;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2111; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 175 GCTGCGCTACATGGTGAAGCAGTGTGAGAGTGGGAGATGAACATTGAGGAGCTGAAGAA 234  
 Db 148 GCTGCGCTACATGGTGAAGCAGTGTGAGAGTGGGAGATGAACATTGAGGAGCTGAAGAA 207  
 QY 235 AAATCTGGAGTACACAGCTTCTCTCTGGAAGCCGCTTACATAGATGAGACACGCAAT 294  
 Db 208 AAATCTGGAGTACACAGCTTCTCTCTGGAAGCCGCTTACATAGATGAGACACGCAAT 267  
 QY 295 CTTGACACGAGGAGGAGCTGCGGCTGAGATGCGGCTGCGGCTGCGGCTGCGGCTGCGG 354  
 Db 268 CTTGACACGAGGAGGAGCTGCGGCTGAGATGCGGCTGCGGCTGCGGCTGCGGCTGCGG 327  
 QY 355 GGACTGCGCTGCGCTCCACCTTCCACCCAGCAGCCGCGGCAAGCCGCCGAGCAGAGA 414  
 Db 328 GGACTGCGCTGCGCTCCACCTTCCACCCAGCAGCCGCGGCAAGCCGCCGAGCAGAGA 387  
 QY 415 GAAGCCCAAGTTCCGAAGCATTGTGCAGCTGTGCAGGCTGGGATCTTCGTGGACCGAT 474  
 Db 388 GAAGCCCAAGTTCCGAAGCATTGTGCAGCTGTGCAGGCTGGGATCTTCGTGGACCGAT 447  
 QY 475 GTTCCGGAGAACATACCTCTGTGGGCCCACTTACTCTACTCGGCTTCTCAACTGTCT 534

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Db 448 GTTCCGGAGAACATACACCTCTGTGGGCCCCACTTACTCTACTGCGGTTCTCAACTGTCT 507
QY 535 CAAGAACTGGAGTCTCTGTGTGTGTGATGTCCTTTTCCCTTTGAACACGAGGACGAGATGACCA 594
Db 508 CAAGAACTTTGGATCTCTGTGTGTGTGATGTCCTTTTGAACACGAGGACGAGATGACCA 567
QY 595 TGCCCTTGAGGACCAATTTTGTGTGTGTGTGATGTCCTTTTGAACACGAGGACGAGATGACCA 654
Db 568 TGCCCTTGAGGACCAATTTTGTGTGTGTGTGATGTCCTTTTGAACACGAGGACGAGATGACCA 627
QY 655 GATTCCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 714
Db 628 GATTCCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 687
QY 715 CAAGAACTTTTACCAACACGATCCACGACGCGATGTTTACCGACAGAGTCCATTTGCTT 774
Db 688 CAAGAACTTTTACCAACACGATCCACGACGCGATGTTTACCGACAGAGTCCATTTGCTT 747
QY 775 CTTGCTCCGACAGAGGATGGTCACTGCTGTGCGAGATTGAGCTTCCCTGGCCATCATCTT 834
Db 748 CTTGCTCCGACAGAGGATGGTCACTGCTGTGCGAGATTGAGCTTCCCTGGCCATCATCTT 807
QY 835 TGTCTCAGCTATTCATGATTATGAGCACACGCGCACTACCAACAGCTTCCACATCCAGAC 894
Db 808 TGTCTCAGCTATTCATGATTATGAGCACACGCGCACTACCAACAGCTTCCACATCCAGAC 867
QY 895 CAACTCAGATGTGCCATGCTTACAAATGATGCTTCACTGCTGGAATCAACATCAG 954
Db 868 CAACTCAGATGTGCCATGCTTACAAATGATGCTTCACTGCTGGAATCAACATCAG 927
QY 955 CTCCTGTTTCCGATTTGATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1014
Db 928 CTCCTGTTTCCGATTTGATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 987
QY 1015 TGAGTTTTCAGACTCCGAGCCCTGTCTATGATGATGATGATGATGATGATGATGATGATGATG 1074
Db 988 TGAGTTTTCAGACTCCGAGCCCTGTCTATGATGATGATGATGATGATGATGATGATGATGATG 1047
QY 1075 CAACTTCCAGAGTGAAGACCATGAAGACACGCTTGCAACAGCTTGGAGAGATTGACAA 1134
Db 1048 CAACTTCCAGAGTGAAGACCATGAAGACACGCTTGCAACAGCTTGGAGAGATTGACAA 1107
QY 1135 GCCCAAGGCCCTGTCTACTGCTCATGCTGCTGACATFAGCCACCAACCAACAGCAGT 1194
Db 1108 GCCCAAGGCCCTGTCTACTGCTCATGCTGCTGACATFAGCCACCAACCAACAGCAGT 1167
QY 1195 GTTGTTCACAGCCGTTGGACCAAGGCCCTCATGAGGAAATTTCTCCGTCAGGGTGACAA 1254
Db 1168 GTTGTTCACAGCCGTTGGACCAAGGCCCTCATGAGGAAATTTCTCCGTCAGGGTGACAA 1227
QY 1255 GGAGGCAGAGTTGGGCCCTGCCCTTTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1314
Db 1228 GGAGGCAGAGTTGGGCCCTGCCCTTTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1287
QY 1315 ACAGTCTCAGATAGGTTTCATGACTTTCATGAGGAGCCACATTTCTGTGCTGACTGA 1374
Db 1288 ACAGTCTCAGATAGGTTTCATGACTTTCATGAGGAGCCACATTTCTGTGCTGACTGA 1347
QY 1375 CFTGGCAGAGAAGAGTTTCAGCCCTCGCGCATCAGGACTCCAAAGTCTAAACACGACC 1434
Db 1348 CFTGGCAGAGAAGAGTTTCAGCCCTCGCGCATCAGGACTCCAAAGTCTAAACACGACC 1407
QY 1435 CAGCTTTCAGTGGCCGACCCCTCTCTGATGCTGAGTGGAGGAGCCCAACCCCTGAGCT 1494
Db 1408 CAGCTTTCAGTGGCCGACCCCTCTCTGATGCTGAGTGGAGGAGCCCAACCCCTGAGCT 1467
QY 1495 GCTCAGCTTTCCTTCCACTGGGTCAAGCCGATTCAGAGAAATTAAGAGAAATGAAGGA 1554
Db 1468 GCTCAGCTTTCCTTCCACTGGGTCAAGCCGATTCAGAGAAATTAAGAGAAATGAAGGA 1527
QY 1555 ACGGGCAGCAAGTGGCATCAACCAACAGATGCCATTTGACGAGCTGTCCCTCTGTGAAGA 1614
Db 1528 ACGGGCAGCAAGTGGCATCAACCAACAGATGCCATTTGACGAGCTGTCCCTCTGTGAAGA 1587
1615 :AGAGCCCCCCCCCATCCCTGCCGAGATGAACAAACAGAAATGGGAATCTGGATTAGCC 1674
1588 :AGAGCCCCCCCCCATCCCTGCCGAGATGAACAAACAGAAATGGGAATCTGGATTAGCC 1647
1675 :TGGGGCTGGCCCGAGGCTTTCATTGAGTCCAAAGTGTGTTGATGTCATCAGCACCATTCCAT 1734
1648 :TGGGGCTGGCCCGAGGCTTTCATTGAGTCCAAAGTGTGTTGATGTCATCAGCACCATTCCAT 1707
1735 :AGAGCTGGCTCCCCCATCTCTCAAGGAGAGCTGTGCTGTTGGAAGAAACAAACACCATG 1794
1708 :AGAGCTGGCTCCCCCATCTCTCAAGGAGAGCTGTGCTGTTGGAAGAAACAAACACCATG 1767
1795 :AAGGCAAAATCCAGAGATTTTGGGTTGGGAAAGGGCCCCCTCCACCTCAGACCCACT 1854
1768 :AAGGCAAAATCCAGAGATTTTGGGTTGGGAAAGGGCCCCCTCCACCTCAGACCCACT 1827
1855 :GGGGTGCATTTAATGTTCCGCGCAGCAGACTGGGAACTTCAGGCTCCCACTGGTCACT 1914
1828 :GGGGTGCATTTAATGTTCCGCGCAGCAGACTGGGAACTTCAGGCTCCCACTGGTCACT 1887
1915 :GTGCCCCATCCCTCAGCCTCTGGATTCTTCTCATGCGCAGCTGGCTGCCAGGAGCGGGA 1974
1888 :GTGCCCCATCCCTCAGCCTCTGGATTCTTCTCATGCGCAGCTGGCTGCCAGGAGCGGGA 1947
1975 :GTTTCTGGAGGCTTCCAGGCGCTTGGGAAAGGCTCAGAGATCCAGAGCCCCCTGGAGCC 2034
1948 :GTTTCTGGAGGCTTCCAGGCGCTTGGGAAAGGCTCAGAGATCCAGAGCCCCCTGGAGCC 2007
2035 :TCCCCCATCTTTTGGCTTCCAGTTCCTAAGTTCCTAAGCAATACATTTTGGGGTTCCTTCAGCCC 2094
2008 :TCCCCCATCTTTTGGCTTCCAGTTCCTAAGTTCCTAAGCAATACATTTTGGGGTTCCTTCAGCCC 2067
2095 :CCACCCAGATCTTAGCTGCGAGCTGTGGTGCCCTTTTCTCCCTTGGGAAAGGCTG 2154
2068 :CCACCCAGATCTTAGCTGCGAGCTGTGGTGCCCTTTTCTCCCTTGGGAAAGGCTG 2127
2155 :GAATAGGATAGAAAGCTGGGGTTTTCAGAGCCCTATGTGTGGGAGGGGAGTGGATTC 2214
2128 :GAATAGGATAGAAAGCTGGGGTTTTCAGAGCCCTATGTGTGGGAGGGGAGTGGATTC 2187
2215 :TTCAGGCGATGTTACCTTTCTAGGATCTGGGAATGGGTGGAGAGGACATCTCTTCACC 2274
2188 :TTCAGGCGATGTTACCTTTCTAGGATCTGGGAATGGGTGGAGAGGACATCTCTTCACC 2247
2275 :CCAGAAATGCGCTGCTTC 2292
2248 :CCAGAAATGCGGGAATTC 2265
RESULT 4
AAQ83969
ID AAQ83969 standard; cDNA; 1844 BP.
XX AAQ83969;
XX AC AAQ83969;
XX DT 25-MAR-2003 (updated)
XX DT 11-OCT-1995 (first entry)
XX XX Cyclic-GMP stimulated nucleotide PDE clone p12-3a.
XX KW Cyclic-GMP stimulated nucleotide phosphodiesterase;
XX KW bovine brain; hormones; neurotransmitters; transmission regulation;
XX KW antibodies; enzyme purification; clone p12-3a; ss.
XX OS Bos taurus.
XX FH Key
XX FT CDS
XX FT 114..1718
XX PN /*tag= a
XX US538957.7-A.
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Db	1838	CCGAAG 1843		QY	GGACTGGCTGGCTCCACCTTACCCAGCAGGCGCGGCCCAAGGCCCGCCGAGCAGAGGA 414
Db				Db	GGACTGGCTGGCTCCACCTTACCCAGCAGGCGCGGCCCAAGGCCCGCGAG --CGAAGA 460
RESULT 5				QY	GAAGCCCAAGTTCGGAAGCATTGTGCAGCTGTGCAGCTGGGATCTTCGTGGAGCAGAT 474
AAT67200				Db	GAAGCCCAAGTTCGGAAGCATTGTGCAGCTGTGCAGCTGGGATCTTCGTGGAGCAGAT 520
XX				QY	GTTCGGGAGAACATACACCTCTGTGGGCCCACTTACTCTACTCTGGGTCTTCAACTGTCT 534
XX				Db	GTTCGGGAGAACATACACCTCTGTGGGCCCACTTACTCTACTCTGGGTCTTCAACTGTCT 580
DT	25-MAR-2003	(updated)		QY	GAAGAACTGTATCTGTGGCTGTGATCTCTTTTCTTTGAACAGGAGCAGATGACCA 594
DT	31-JUL-1997	(first entry)		Db	GAAGAACTGTATCTGTGGCTGTGATCTCTTTTCTTTGAACAGGAGCAGATGACCA 640
XX				QY	TGCCCTGAGGACCAATGTTTGTGAGTGTGCTGACTCGGCAATCACTCATCAGCCCTTCAA 654
XX				Db	TGCCCTGAGGACCAATGTTTGTGAGTGTGCTGACTCGGCAATCACTCATCAGCCCTTCAA 700
KW				QY	GATTCCCACTGTGTTTGTGAGTGTGCTGCTGGATGCTTGGAGACAGCTATGGAAGTA 714
KW				Db	GATTCCCACTGTGTTTGTGAGTGTGCTGCTGGATGCTTGGAGACAGCTATGGAAGTA 760
FT				QY	CAAGAATCCTTACCACACACAGATCCAGCGACCGATGTTTACCAGACAGTCCATTCGTT 774
FT				Db	CAAGAATCCTTACCACACACAGATCCAGCGACCGATGTTTACCAGACAGTCCATTCGTT 820
XX				QY	CTTGCTCGCACAGGATGTTGCTGCTGCTGAGATGAGTGTCTGCTGCTGCTGCTGCTGCT 834
XX				Db	CTTGCTCGCACAGGATGTTGCTGCTGCTGAGATGAGTGTCTGCTGCTGCTGCTGCTGCT 880
PR	20-APR-1992;	92US-0872644.		QY	TGCTGCAGCTATCCATGATATGAGCACACCGGCACTACCAACAGCTTCCACATCCAGAC 894
PR	19-APR-1991;	91US-0688356.		Db	TGCTGCAGCTATCCATGATATGAGCACACCGGCACTACCAACAGCTTCCACATCCAGAC 940
XX				QY	CAAGTCAGAATGTGCCATCGTGTACATGATGATGATGATGATGATGATGATGATGATGAT 954
XX				Db	CAAGTCAGAATGTGCCATCGTGTACATGATGATGATGATGATGATGATGATGATGATGAT 1000
XX				QY	CTCTGTTTCCGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014
XX				Db	CTCTGTTTCCGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1060
PS	Claim 3;	Column 55-60;	69pp; English.	QY	TGAGTTTGTAGAACTCCGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
CC				Db	TGAGTTTGTAGAACTCCGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1120
CC				QY	CCATTTCACCAAGTGAAGCATTGAGACAGCCTTGCACAGCTGGAGAGGATGACAA 1134
CC				Db	CCATTTCACCAAGTGAAGCATTGAGACAGCCTTGCACAGCTGGAGAGGATGACAA 1180
CC				QY	GCCCAAGCCCTGCTCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
CC				Db	GCCCAAGCCCTGCTCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240
XX				QY	GTTGGTCCACAGCGTTGGACCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1254
XX				Db	GTTGGTCCACAGCGTTGGACCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1300
QY	175	GCTGGCTACATGCTGAGCAGTGGAGATGGAGAGATAAATGAGGAGCTGAAGAA 234		QY	GGAGGACAGATGGGCTGCGCTTTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1314
Db	224	GCTGGCTACATGCTGAGCAGTGGAGATGGAGAGATAAATGAGGAGCTGAAGAA 283		Db	GGAGGCTGAGCTGGGCTGCGCTTTTCTCCGCTCTGTGACCGCACTTCCACTCTAGTGGC 1360
QY	235	AAATCTGGAGTACACAGCTTCTGCTGGAAGCCGCTTACATAGATGAGACACCGCAAT 294		QY	ACAGTCTCAGATAGGCTTCTATGCTGAGTGGAGCCCACTTCTCTGTGCTGACTGA 1374
Db	284	AAACCTGGAGTACACAGCTTCTGCTGGAAGCCGCTTACATAGATGAGACACCGCAAT 343		Db	GCAGTCCAGATAGGCTTCTATGCTGAGTGGAGCCCACTTCTCTGTGCTGACTGA 1420
QY	295	CTTGACACGGAGGAGCTGACAGGAGCTGCGGTGAGATGCGGCTTCCGAGGTGCG 354		QY	CGTGGCAGAGAGAGTGTTCAGCCCTTGGGGGAGTGGAGGAGTCCCAAGTCTTAAAAACAGCC 1434
Db	344	CCTGGACACGGAGGAGTACAGTGCAGAGAGCTGCGGTGAGTGGCTTCCAGAGGTGCG 403		Db	TGTGGCTGAGAAGAGTGTCCAGCCCTGCGGGGAGGAGTGCAGAGTCTAAAAACAGCC 1480

Query Match 43.6%; Score 1347.6; DB 18; Length 1844;  
 Best Local Similarity 90.6%; Pred. No. 0;  
 Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

QY 175 GCTGGCTACATGCTGAGCAGTGGAGATGGAGAGATAAATGAGGAGCTGAAGAA 234  
 |||||  
 Db 224 GCTGGCTACATGCTGAGCAGTGGAGATGGAGAGATAAATGAGGAGCTGAAGAA 283  
 |||||  
 QY 235 AAATCTGGAGTACACAGCTTCTGCTGGAAGCCGCTTACATAGATGAGACACCGCAAT 294  
 |||||  
 Db 284 AAACCTGGAGTACACAGCTTCTGCTGGAAGCCGCTTACATAGATGAGACACCGCAAT 343  
 |||||  
 QY 295 CTTGACACGGAGGAGCTGACAGGAGCTGCGGTGAGATGCGGCTTCCGAGGTGCG 354  
 |||||  
 Db 344 CCTGGACACGGAGGAGTACAGTGCAGAGAGCTGCGGTGAGTGGCTTCCAGAGGTGCG 403

The present sequence encodes a 63 kDa Ca<sup>2+</sup>/calmodulin-stimulated cyclic nucleotide phosphodiesterase (Cam-PDE) enzyme derived from bovine brain. The DNA sequences are used for the production of the recombinant enzymes, which in turn may be used for antibody production and to screen for compounds that modulate phosphodiesterase activity.

(Updated on 25-MAR-2003 to correct PF field.)  
 (Updated on 25-MAR-2003 to correct PI field.)

Sequence 1844 BP; 417 A; 551 C; 514 G; 362 T; 0 other;

Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;

WPI; 1997-131799/12.

P-PSDB; AAW18038.

DNA encoding bovine and human phosphodiesterase enzymes - stimulated by calcium/calmodulin, useful for recombinant prodn. of the enzymes

Claim 3; Column 55-60; 69pp; English.

The present sequence encodes a 63 kDa Ca<sup>2+</sup>/calmodulin-stimulated cyclic nucleotide phosphodiesterase (Cam-PDE) enzyme derived from bovine brain. The DNA sequences are used for the production of the recombinant enzymes, which in turn may be used for antibody production and to screen for compounds that modulate phosphodiesterase activity.

(Updated on 25-MAR-2003 to correct PF field.)  
 (Updated on 25-MAR-2003 to correct PI field.)

Sequence 1844 BP; 417 A; 551 C; 514 G; 362 T; 0 other;







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QY 475 GTTCGGAGAACATACACCTCTGTGGGCCCCACCTTACTCTACTGTGGGTCTCAACTGTCT 534
DB 521 GTTCGGAGAACATACACCTCTGTGGGCCCCACCTTACTCTACTGTGGGTCTCAACTGTCT 580
QY 535 CAAGAACCTGATCTCTGGTCTGTGTGATGTCTTTTCTTGAACAGGAGCAGATGACCA 594
DB 581 CAAGAACCTGATCTCTGGTCTGTGTGATGTCTTTTCTTGAACAGGAGCAGATGACCA 640
QY 595 TGCCCTGAGGACCATGTGTTTGTAGTCTGCTGACCTGGCATACCTCATCAGCCGCTCAA 654
DB 641 CGCCCTGAGGACCATGTGTTTGTAGTCTGCTGACCTGGCATACCTCATCAGCCGCTCAA 700
QY 655 GATTCCTGCTGTTTGTAGTCTGCTGATGCTTCTGGATGCTTGGAGACAGCTATGGAAGTA 714
DB 701 GATTCCTGCTGTTTGTAGTCTGCTGATGCTTCTGGATGCTTGGAGACAGCTATGGAAGTA 760
QY 715 CAAGAACTCTTACACAAACAGATCCAGCGAGCGATGTTTACCCAGACAGTCCATGTGTT 774
DB 761 CAAGAACTCTTACACAAACAGATCCAGCGAGCTGACGTCACCCAGAGCGTCCATGCTT 820
QY 775 CTTCCTCCGACAGGATGTGCTGCTGCTGCGAGATTGAGCTCTCTGCGCATCATCTT 834
DB 821 CTTCCTCCGACAGGATGTGCTGCTGCTGCGAGATTGAGCTCTCTGCGCATCATCTT 880
QY 835 TGCTGCGAGTATCCATGATATGAGCACACGCGGACTTACCACAGCTTCCACATCCAGAC 894
DB 881 TGCTGCGAGTATCCATGATATGAGCACACGCGGACTTACCACAGCTTCCACATCCAGAC 940
QY 895 CAAGTCAGATGTGCGCATCTGTGTACATGATGCTGTGAGTGTGAGAGATCACCACATCAG 954
DB 941 CAAGTCAGATGTGCGCATCTGTGTACATGATGCTGTGAGTGTGAGAGATCACCACATCAG 1000
QY 955 CTCGTTTTCCGATGATGAGGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1014
DB 1001 CTCGTTTTCCGATGATGAGGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1060
QY 1015 TGAGTTTGTAGAACTCCGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074
DB 1061 TGAGTTTGTAGAACTCCGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120
QY 1075 CCATTCAGCAAGTGAAGACCATGAGACAGCCTTGCAACAGCTGGAGAGATGACAA 1134
DB 1121 CCATTCAGCAAGTGAAGTCCATGAGACAGCCTTGCAACAGCTGGAGAGATGACAA 1180
QY 1135 GCCAAGGCCCTGCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
DB 1181 GTCCAAGGCCCTGCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
QY 1195 GTTGGTCCACAGCCGTTGGACCAAGGCCCTCATGAGGAAATTTTCCGTCAGGCTGACAA 1254
DB 1241 GTCGGTTCACAGCCGTTGGACCAAGGCCCTCATGAGGAAATTTTCCGTCAGGCTGACAA 1300
QY 1255 GGAGGACAGATTGGGCTGGCCCTTTTCTCCACTCTGTGACCGCATCTCCACTAGTGGC 1314
DB 1301 GGAGGCTGAGCTGGGCTGGCCCTTTTCTCCGCTCTGTGACCGCATCTCCACTAGTGGC 1360
QY 1315 ACAGTCTCAGATAGGTTTCATCGACTTCATGCTGAGCCCATCTCTGCTGCTGCTGCTGCTG 1374
DB 1361 CAGTGTCCAGATAGGTTTCATCGACTTCATGCTGAGCCCATCTCTGCTGCTGCTGCTGCTG 1420
QY 1375 CGTGGCAGAGAGATGTTCAGCCCTTGCGGAGTGGAGCTTCAAGCTTCAAAACACGACC 1434
DB 1421 TGTGGCTGAGAGAGTGTTCAGCCCTTGCGGAGTGGAGCTTCAAGCTTCAAAACACGACC 1480
QY 1435 CAGCTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGGAGACCCCAACCTGTATGT 1494
DB 1481 CAGCTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGGAGACCCCAACCTGTATGT 1540
QY 1495 GGTGAGCTTTCGTTCCACCTGGGTCACCGCATTCAGGAGATTAAGCAGAAATGAAGGA 1554
DB 1541 GGTGAGCTTTCGTTCCACCTGGGTCACCGCATTCAGGAGATTAAGCAGAAATGAAGGA 1600
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QY 1555 ACGGCGAGCAAGTGGCATGCACCAACAGATGTCCATTTGACGAGTGTCCCTCTGTGAAGA 1614
DB 1601 ACGGCGCGAGCGGCATGCACCAACAGATGTCCATTTGACGAGTGTCCCTCTGTGAAGA 1660
QY 1615 AGAGGCCCGCCATCCCTGCGGAGATGAACACCAACAGATGGGAATCTGGATTAGCC 1674
DB 1661 AGAGGCCCGCCATCCCTGCGGAGATGAACACCAACAGATGGGAATCTGGATTAGCC 1719
QY 1675 CTGGGCTGCGCCAGGTCTTCTATTGAGTCCAAAGTGTGTTGATGTCATCAGCACCATCCAT 1734
DB 1720 --GGGGCTGGCCAGGTCTCTCAGTGAGTCTCTGAGTGTTCGATGTCATCAGCACCATCCAT 1777
QY 1735 CAGGACTGGCTCCCGCATCTCTCCAAAGGAGCGGTG---GTCTGTGAAGAACAACCCAC 1791
DB 1778 CGGACTGGCTCCCGCATCTCTCCGAGGCGAATGGATGTCAAGGAACAAGAAACCCAC 1837
QY 1792 CTGAAG 1797
DB 1838 CCGAAG 1843
```

RESULT 8  
AAV54753  
ID AAV54753 standard; cDNA; 1844 BP.  
AC AAV54753;  
XX  
DT 29-OCT-1998 (first entry)  
XX  
DE 63 kDa CaM-PDE DNA from clone p12.3a.  
XX  
KW Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; CaM-PDE;  
KW assay; identification; modification; enzymatic activity; modulator; ss.  
XX Bos sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 114..1718  
FT */\*tag= a*  
FT */product= CaM-PDE*  
XX  
PN US8000987-A.  
XX  
PD 01-SEP-1998.  
XX  
PF 31-MAY-1995; 95US-0455525.  
XX  
PR 20-APR-1992; 92US-0872644.  
PR 19-APR-1991; 91US-0688356.  
PR 29-AUG-1994; 94US-0297494.  
PR 31-MAY-1995; 95US-0455525.  
XX (UNIW ) UNIV WASHINGTON.  
PA  
XX Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;  
PI WPI; 1998-494762/42.  
XX P-PSDB; AAV71223.  
DR  
XX  
PT Identification of modulators of Calcium/calmodulin sensitive cyclic  
PT nucleotide phosphodiesterase - uses recombinant cells expressing the  
PT enzyme and monitoring protein expression in the presence of  
PT potential modulators  
XX  
PS Example 3; Columns 55-58; 69pp; English.  
XX  
CC The present sequence encodes the 63 kDa Ca2+/calmodulin sensitive cyclic  
CC nucleotide phosphodiesterase (CaM-PDE) from bovine brain. CaM-PDE enzymes  
CC catalyze the hydrolysis of cyclic nucleotides and as such control their  
CC intracellular level. They are controlled by second messengers e.g. Ca2+  
CC and calmodulin and transmembrane signals and through pathways involving  
CC these, regulate flow of information from extracellular hormones,  
CC neurotransmitters and other signals using cyclic nucleotides as

CC messengers. The specification describes an assay for identifying a  
 CC chemical agent which modifies the enzymatic activity of a mammalian  
 CC Cam-PDE. The assays are useful for identifying modulators of Cam-PDEs.  
 CC The assay is carried out by incubating cells expressing Cam-PDE with the  
 CC suspected modulator and measuring its effect e.g. monitoring the  
 CC hydrolysis of cAMP and/or cGMP.

XX Sequence 1844 BP; 417 A; 551 C; 514 G; 362 T; 0 other;

Query Match 43.6%; Score 1347.6; DB 19; Length 1844;  
 Best Local Similarity 90.6%; Pred. No. 0;  
 Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

Qy 175 GGTGCTACATGGTGAAGCAGTTGGAGAAATGGGAGATGAACATTTAGGAGCTGAAGAA 234  
 Db 224 GGTGCTACATGGTGAAGCAGTTGGAGAAATGGGAGATGAACATTTAGGAGCTGAAGAA 283  
 Qy 235 AAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTACATAGATGAGACACGCAAT 294  
 Db 284 AAACCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTATATAGATGAGACTCGGCAAT 343  
 Qy 295 CTGGACACGAGGAGAGCTGCAGAGCTGCGGTTCAGATGCGCTTCGGAGGTGCG 354  
 Db 344 CTGGACACGAGGAGATGAGCTGCAGAGCTGCGGTTCAGATGCGCTTCAGAGGTGCG 403  
 Qy 355 GGAATGGCTGCGCTCCACCTTCACCCAGCAGCCGCGGCAAGAGCCGCGAGAGGA 414  
 Db 404 GGAATGGCTGCGCTCCACCTTCACCCAGCAGCCGCGGCAAGAGCCGCGAGAGGA 460  
 Qy 415 GAAGCCCAAGTTCCGGAACATTTGTCAGCGCTGTCAGCTGGGATCTTCGTGAACGAT 474  
 Db 461 GAAGCCCAAGTTCCGGAACATTTGTCAGCGCTGTCAGCTGGGATCTTCGTGAACGAT 520  
 Qy 475 GTTCGGGAGAACATACCTCTGTGGGCCCACTTACTCTACTTGGGGTTCCTCACTGCT 534  
 Db 521 GTTCGGGAGAACATACCTCTGTGGGCCCACTTACTCTACTTGGGGTTCCTCACTGCT 580  
 Qy 535 CAAGAATCTGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594  
 Db 581 CAAGAATCTGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640  
 Qy 595 TGCCCTGAGGACCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654  
 Db 641 CGCCCTGAGGACCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700  
 Qy 655 GATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714  
 Db 701 GATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760  
 Qy 715 CAAGAATCTTACCAACACAGATCCAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774  
 Db 761 CAAGAATCTTACCAACACAGATCCAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 820  
 Qy 775 CTGCTCCGACAGGATGGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 834  
 Db 821 CTGCTCCGACAGGATGGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880  
 Qy 835 TGCT 894  
 Db 881 TGCT 940  
 Qy 895 CAAGTCAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954  
 Db 941 CAAGTCAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000  
 Qy 955 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014  
 Db 1001 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1060  
 Qy 1015 TGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074  
 Db 1061 TGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1120

Qy 1075 CCATTTCCAGCAAGTGAAGACCATGAAGACAGACAGCCTTCCAAACAGCTGGAGGATTGACAA 1134  
 Db 1121 CCATTTCCAGCAAGTGAAGTCCATGAAGACAGACAGCCTTCCAAACAGCTGGAGGATTGACAA 1180  
 Qy 1135 CCAAGGCGCTCTCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194  
 Db 1181 CCAAGGCGCTCTCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240  
 Qy 1195 CTTGCTCCAGCAGCGCTTGGACCAAGGCGCTTCATGAGGAAATTTCTCCGTCAGGCTGACAA 1254  
 Db 1241 CTTGCTCCAGCAGCGCTTGGACCAAGGCGCTTCATGAGGAAATTTCTCCGTCAGGCTGACAA 1300  
 Qy 1255 GGAGCAGAGTTGGGCGCTGCGCTTTCTCCACTCTGTGACGCGACTTCCACTCTAGTGGC 1314  
 Db 1301 GGAGCAGAGTTGGGCGCTGCGCTTTCTCCACTCTGTGACGCGACTTCCACTCTAGTGGC 1360  
 Qy 1315 ACAGTCTCAGATAGGTTTCATCGACTTCATTGTTGGAGCCACATTTCTCTGCTGCTGCTGCTGCT 1374  
 Db 1361 ACAGTCTCAGATAGGTTTCATCGACTTCATTGTTGGAGCCACATTTCTCTGCTGCTGCTGCTGCT 1420  
 Qy 1375 CTTGTCAGAGAGAGTCTTCCAGCCCTTGGCGGATGAGGACTCCAAAGTCTTAAACACGAC 1434  
 Db 1421 CTTGTCAGAGAGAGTCTTCCAGCCCTTGGCGGATGAGGACTCCAAAGTCTTAAACACGAC 1480  
 Qy 1435 CAGCTTTAGTGGCGCGCTCTCTCTGATGTTGGAAGTGGAGACCCCAACCTGATGT 1494  
 Db 1481 CAGCTTTAGTGGCGCGCTCTCTCTGATGTTGGAAGTGGAGACCCCAACCTGATGT 1540  
 Qy 1495 GGTGAGCTTGTGTCAGCTGGTCAAGCCGCTTCCAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 1554  
 Db 1541 GGTGAGCTTGTGTCAGCTGGTCAAGCCGCTTCCAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 1600  
 Qy 1555 ACAGGAGAGAGTGGGATCAACCAAGATGTTCCATGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1614  
 Db 1601 ACAGGAGAGAGTGGGATCAACCAAGATGTTCCATGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1660  
 Qy 1615 AGAGGCGCGCGCT 1674  
 Db 1661 AGAGGCGCGCGCT 1719  
 Qy 1675 CTGGGCT 1734  
 Db 1720 CTGGGCT 1777  
 Qy 1735 CAGGACTGCT 1791  
 Db 1778 CAGGACTGCT 1837  
 Qy 1792 CTGAAG 1797  
 Db 1838 CCGAAG 1843

## RESULT 9

AAV36148  
 ID AAV36148 standard; cDNA; 1844 BP.

XX AAV36148;

XX 07-SEP-1998 (first entry)

XX Bovine Cam-PDE cDNA encoding a 63 kda protein.

XX Bovine; increase; intracellular concentration; cAMP; cGMP;  
 XX calcium ion/calmodulin stimulated cyclic nucleotide phosphodiesterase;  
 XX Cam-PDE; therapy; prognosis; diagnosis; specific modulator;  
 XX Cam-PDE activity; identification; signalling; extracellular hormone;  
 XX neurocrasmitter; selective inhibitor; cardiotoxic; antidepressant;  
 XX antihypertensive; antithrombotic agent; ss.

XX Bos sp.

XX Key Location/Qualifiers

XX Key





Db 1181 GTCAAGGCCCTCTCTGCTGCTTCACTGCTGACATCAGCACCCACCAAGCAGTG 1240  
 QY 1195 GTTGTTCACAGCGTGGACCAAGGCCCTCATGGAGGAATCTTCCGTAGGTGACAA 1254  
 Db 1241 GTCGGTTCACAGCGCTGGACCAAGGCCCTCATGGAGGAATCTTCCGCCAGGTGACAA 1300  
 QY 1255 GGAGCGAGAGTGGCGCTGCTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1314  
 Db 1301 GGAGCGAGAGTGGCGCTGCTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1360  
 QY 1315 ACAGTCTCAGATAGGTTTCATGCACTTCTGTGAGCGCCACATCTCTGTGCTGACATGA 1374  
 Db 1361 GCAGTCCAGAGTGGTTCATGCACTTCTGTGAGCGCCACATCTCTGTGCTGACATGA 1420  
 QY 1375 CGTGCAGAGAGAGTGTTCAGCCCTGCGGAGTACAGACCTCAAGTCTAAACACGACC 1434  
 Db 1421 TGTGCTGAGAGAGTGTTCAGCCCTGCGGAGTACAGACCTCAAGTCTAAACACGACC 1480  
 QY 1435 CAGCTTTTCAGTGGCGCCAGCCCTCTCTGATGTGGAAGTGGAGACCCCAACCCCTGATGT 1494  
 Db 1481 CAGCTTCCAGTGGCGCCAGCCCTCTCTGATGTGGAAGTGGAGACCCCAACCCCTGATGT 1540  
 QY 1495 GGTGAGCTTCTGCTCCAGCTGGTCAAGCGCATTCAGGAGAAATAGCAGAAATGAAGGA 1554  
 Db 1541 GGTGAGCTTCTGCTCCAGCTGGTCAAGCGCATTCAGGAGAAATAGCAGAAATGAAGGA 1600  
 QY 1555 ACGGCGAGCAAGTGGCATCACCAACAGATGTCCATTCAGCAGCTGTCCCTGTGAAGA 1614  
 Db 1601 ACGGCGAGCGGCGCATCACCAACAGATGTCCATTCAGCAGCTGTCCCTGTGAAGA 1660  
 QY 1615 AGAGGCCCCCTATCCCTGCGGAAGATGAACCAACAGAAATGGGAATCTGGATAGCC 1674  
 Db 1661 AGAGGCCCCCTATCCCTGCGGAAGATGAACCAACAGAAATGGGAATCTGGATAGCC 1719  
 QY 1675 CTGGGCTGGCCCGAGTCTTCATGAGTCCAAAGTGTGATGTCATCAGACCATTCAT 1734  
 Db 1720 --GGGCGTGGCCCGAGTCTTCATGAGTCCAAAGTGTGATGTCATCAGACCATTCAT 1777  
 QY 1735 CAGGACTGGCTCCCGCATCTGCTCAAGGGAGCGTG---GTCTGGAGAGAAACACCCAC 1791  
 Db 1778 CCGGACTGGCTCCCGCATCTGCTCGAGGGCGAATGGATGTCAAGGAACAGAAACCCAC 1837  
 QY 1792 CTGAAG 1797  
 Db 1838 CCGAAG 1843

RESULT 11

ABX78849  
 ID ABX78849 standard; cDNA; 1844 BP.  
 AC ABX78849;  
 XX  
 DT 15-APR-2003 (first entry)  
 DE Bovine brain cDNA encoding 63kDa CaM-PDE variant #1.  
 DE  
 XX  
 KW Cow; ss: Ca2+/calmodulin stimulated phosphodiesterase;  
 KW CaM-PDE; 59kDa CaM-PDE; 61kDa CaM-PDE; 63kDa CaM-PDE; CGS-PDE;  
 KW cyclic-GMP-stimulated phosphodiesterase; cardiotonic agent;  
 KW antipressant; anti-hypertensive; anti-thrombotic.  
 XX  
 OS Bos taurus.  
 XX  
 PN US2002151024-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 18-JUN-2001; 2001US-0883825.  
 XX  
 PR 20-APR-1992; 92US-0872644.  
 PR 31-MAY-1995; 95US-0455526.  
 PR 28-JUL-1998; 98US-0123783.

PR 19-APR-1991; 91US-0688356.  
 XX (UNIW ) UNIV WASHINGTON.  
 PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;  
 XX WPI; 2003-198291/19.  
 DR P-PSDB; ABU58716.  
 XX  
 PT New purified and isolated DNA sequence encoding a mammalian  
 PT calcium/calmodulin- or cyclic GMP-stimulated cyclic nucleotide  
 PT phosphodiesterase polypeptide, useful for therapeutic, diagnostic and  
 PT prognostic applications  
 XX  
 PS Example 3; Page 30-32; 7lpp; English.  
 XX  
 CC The invention relates to purified and isolated polynucleotide sequence  
 CC encoding a mammalian Ca<sup>2+</sup>/calmodulin- or cyclic GMP-stimulated cyclic  
 CC nucleotide phosphodiesterase polypeptide (CaM-PDE and CGS-PDE).  
 CC Also included are a DNA vector comprising the novel DNA sequence, a host  
 CC cell transformed with the polynucleotide sequence, a polypeptide product  
 CC of the expression in the transformed host cell, an antibody specifically  
 CC immunoreactive with the polypeptide and assay methods for identifying a  
 CC chemical agent which modifies the enzymatic activity of a mammalian  
 CC CaM-PDE or CGS-PDE. Disclosed are the cDNA and protein sequences  
 CC of bovine 59kDa CaM-PDE, 61kDa CaM-PDE, 63kDa CaM-PDE, CGS-PDE and  
 CC human 61kDa CaM-PDE and CGS-PDE. The DNA sequence is useful for producing  
 CC a polypeptide having the enzymatic activity of a mammalian CaM-PDE or  
 CC CGS-PDE which is used in therapeutic, diagnostic and prognostic  
 CC applications and in the preparation of antibodies. Isolated chemical  
 CC agents which are inhibitors of PDEs may have anti-depressant, anti-  
 CC hypertensive or anti-thrombotic activities or may be cardiotonic agents.  
 CC The present sequence is a Bovine cDNA (or fragment) encoding a  
 CC CaM-PDE or CGS-PDE of the invention.  
 XX  
 SQ Sequence 1844 BP; 417 A; 551 C; 514 G; 362 T; 0 other;  
 Query Match 43.6%; Score 1347.6; DB 25; Length 1844;  
 Best Local Similarity 90.6%; Pred. No. 0;  
 Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;  
 QY 175 GCTCGCTACATGTTGAAGCAGCTTGGAGAAATGGGAGATAAACATTGAGAGCTGAAGAA 234  
 Db 224 GCTCGCTACATGTTGAAGCAGCTTGGAGAAATGGGAGATAAACATTGAGAGCTGAAGAA 283  
 QY 235 AAATCTGAGTACACAGCTTCTCTCTGGAAGCCCTCTACATAGATGAGACACGCGAAT 294  
 Db 284 AAACCTGGAGTACACAGCTTCTCTCTGGAAGCCCTCTATATAGATGAGACTCGGCAAT 343  
 QY 295 CTGGAACACGAGGACAGCTGCGGTCAGATGCGCTGCGCTTCCGAGGTGCG 354  
 Db 344 CTGGAACACGAGGATGAGCTGCGGTCAGATGCGGTCGCTTCCGAGGTGCG 403  
 QY 355 GACTGTGCTGCTCCACCTTCCACCCAGCAGCCCGGCGCAAGCCCGCAGCAGAGA 414  
 Db 404 GACTGTGCTGCTCCACCTTCCACCCAGCAGCCCGGCGCAAGCCCGCAGCAGAGA 460  
 QY 415 GAAGCCCAAGTTCGCAAGCATTGTCACGCTGTGAGGCTGGATTCGTGGAACGGAT 474  
 Db 461 GAAGCCCAAGTTCGCGAGCATGTCACGCTGTGAGGCTGGATTCGTGGAACGGAT 520  
 QY 475 GTTCCGGAGAAATACACCTCTGTGGGCCCCACTTACTCTACTGCGGTCTCAACTGTCT 534  
 Db 521 GTTCCGGAGAGGTACACCTCTGTGGGCCCCACTTACTCTACTGCGGTCTCAACTGTCT 580  
 QY 535 CAAGAACCTGGATCTCTGGT 594  
 Db 581 CAAGAACCTGGATCTCTGGT 640  
 QY 595 TGCCCTGAGGACCATTTTGT 654  
 Db 641 CGCCCTGAGGACCATTTTGT 700

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655 GATTCCTCCACTGTGTTTTCATGACGTTCTCGATGCGCTTGGAGACAGCGTATGGGAAGTA 714
656 GATTCCTCCACTGTGTTTTCATGACGTTCTCGATGCGCTTGGAGACAGCGTATGGGAAGTA 715
701 GATTCCTCCACTGTGTTTTCATGACGTTCTCGATGCGCTTGGAGACAGCGTATGGGAAGTA 760
702 GATTCCTCCACTGTGTTTTCATGACGTTCTCGATGCGCTTGGAGACAGCGTATGGGAAGTA 761
715 CAGGATCCTTACCAACACAGATCCAGCAGCGATGTTACCCAGACAGTCCATGCTT 774
716 CAGGATCCTTACCAACACAGATCCAGCAGCGATGTTACCCAGACAGTCCATGCTT 775
761 CAGGATCCTTACCAACACAGATCCAGCAGCGATGTTACCCAGACAGTCCATGCTT 820
762 CAGGATCCTTACCAACACAGATCCAGCAGCGATGTTACCCAGACAGTCCATGCTT 821
775 CTTGCTCCCAACAGGATGGTGCATGCTGCTGCGAGATGAGCTCCTGGCCATCATCTT 834
776 CTTGCTCCCAACAGGATGGTGCATGCTGCTGCGAGATGAGCTCCTGGCCATCATCTT 835
821 CTTGCTCCCAACAGGATGGTGCATGCTGCTGCGAGATGAGCTCCTGGCCATCATCTT 880
822 CTTGCTCCCAACAGGATGGTGCATGCTGCTGCGAGATGAGCTCCTGGCCATCATCTT 881
835 TGTGAGCTATCCCATGATATGAGACACACGCGCTACTACCAACAGCTTCCATCCAGAC 894
836 TGTGAGCTATCCCATGATATGAGACACACGCGCTACTACCAACAGCTTCCATCCAGAC 895
881 TGTGAGCTATCCCATGATATGAGACACACGCGCTACTACCAACAGCTTCCATCCAGAC 940
882 TGTGAGCTATCCCATGATATGAGACACACGCGCTACTACCAACAGCTTCCATCCAGAC 941
895 CAAATCGGAATGCGGCATCTCTACAGACGCGCTCAGTGTGGGAATCACCACATCAG 954
896 CAAATCGGAATGCGGCATCTCTACAGACGCGCTCAGTGTGGGAATCACCACATCAG 955
941 CAAATCGGAATGCGGCATCTCTACAGACGCGCTCAGTGTGGGAATCACCACATCAG 1000
942 CAAATCGGAATGCGGCATCTCTACAGACGCGCTCAGTGTGGGAATCACCACATCAG 1001
955 CTCGTGTTTCCGATGTGATGAGATGATGAGATGAACATTTTCATCAACCTCACCAGGA 1014
956 CTCGTGTTTCCGATGTGATGAGATGATGAGATGAACATTTTCATCAACCTCACCAGGA 1015
1001 CTCGTGTTTCCGATGTGATGAGATGATGAGATGAACATTTTCATCAACCTCACCAGGA 1060
1002 CTCGTGTTTCCGATGTGATGAGATGATGAGATGAACATTTTCATCAACCTCACCAGGA 1061
1015 TGAGTTTGTAGAACCTCCGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074
1016 TGAGTTTGTAGAACCTCCGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
1061 TGAGTTTGTAGAACCTCCGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120
1062 TGAGTTTGTAGAACCTCCGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1121
1075 CCATTTTCCAGCAAGTGAAGACCATGAAGACAGCCCTTGAACAGCTGGAGAGATTGACAA 1134
1076 CCATTTTCCAGCAAGTGAAGACCATGAAGACAGCCCTTGAACAGCTGGAGAGATTGACAA 1135
1121 CCATTTTCCAGCAAGTGAAGACCATGAAGACAGCCCTTGAACAGCTGGAGAGATTGACAA 1180
1122 CCATTTTCCAGCAAGTGAAGACCATGAAGACAGCCCTTGAACAGCTGGAGAGATTGACAA 1181
1135 GCGCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
1136 GCGCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1195
1181 GTCGAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
1182 GTCGAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1241
1195 GTTGTGTCACAGCCCTGGACCAAGCCCTCATGAGAGAAATTCCTCGTCAAGGTGACAA 1254
1196 GTTGTGTCACAGCCCTGGACCAAGCCCTCATGAGAGAAATTCCTCGTCAAGGTGACAA 1255
1241 GTCGGTTACAGCCCTGGACCAAGCCCTCATGAGAGAAATTCCTCGTCAAGGTGACAA 1300
1242 GTCGGTTACAGCCCTGGACCAAGCCCTCATGAGAGAAATTCCTCGTCAAGGTGACAA 1301
1255 GCGAGCAGATGTCGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314
1256 GCGAGCAGATGTCGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1315
1301 GAGGCTGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1360
1302 GAGGCTGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1361
1315 ACAGTCTAGATAGGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1374
1316 ACAGTCTAGATAGGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1375
1361 GCGATCCCAAGATGTTGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1420
1362 GCGATCCCAAGATGTTGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1421
1375 COTGCGAGAGAGATGTTTTCAGCCCTGGCGGATGAGAGCTTCAAGTCTTAAACACAGCC 1434
1376 COTGCGAGAGAGATGTTTTCAGCCCTGGCGGATGAGAGCTTCAAGTCTTAAACACAGCC 1435
1421 TGTGCTGAGAAAGTGTCCAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCA 1480
1422 TGTGCTGAGAAAGTGTCCAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCA 1481
1435 CAGCTTTCAGTGGCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1494
1436 CAGCTTTCAGTGGCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1495
1481 CAGCTTTCAGTGGCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1540
1482 CAGCTTTCAGTGGCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1541
1495 GGTACGCTTTCGTTCCACTGGGTCAAGCGCATTCAGAGAAATGAAGCAAGATGGAAGGA 1534
1496 GGTACGCTTTCGTTCCACTGGGTCAAGCGCATTCAGAGAAATGAAGCAAGATGGAAGGA 1535
1541 GGTACGCTTTCGTTCCACTGGGTCAAGCGCATTCAGAGAAATGAAGCAAGATGGAAGGA 1600
1542 GGTACGCTTTCGTTCCACTGGGTCAAGCGCATTCAGAGAAATGAAGCAAGATGGAAGGA 1601
1555 ACGGCGAGCAAGTGGCATCACCAACAGATGCTTCCATGACGAGCTGCTCCCTCTGGAAGA 1614
1556 ACGGCGAGCAAGTGGCATCACCAACAGATGCTTCCATGACGAGCTGCTCCCTCTGGAAGA 1615
1601 ACGGCGGCGAGCGGCATCACCAACAGATGCTTCCATGACGAGCTGCTCCCTCTGGAAGA 1660
1602 ACGGCGGCGAGCGGCATCACCAACAGATGCTTCCATGACGAGCTGCTCCCTCTGGAAGA 1661
1615 AGAGGCGCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1674
1616 AGAGGCGCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1675
1661 AGAGGCGCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1719
1662 AGAGGCGCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1720
1675 CTGGGCTGCGCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1734
1676 CTGGGCTGCGCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1735
1720 --GGGCGCTGGCCAGGCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1777
1721 --GGGCGCTGGCCAGGCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1778
1735 CAGGACTGGCTCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1791
1736 CAGGACTGGCTCCCGCCCTCTCTGATGTGGAAGTGGAGACCCCAAGCCCTGATGT 1792
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Db 1778 CGGACATGGCTCCCGCATCTGCTCCGAGGCGGATGATGTCAGGACAGAAACCCAC 1837

QY 1792 (TGAAG 1797

Db 1838 (CGAAG 1843

RESULT 12

AAQ30175

ID AAQ30175 standard; DNA; 1844 BP.

XX AAQ30175;

AC AC

XX 25-MAR-2033 (updated)

DT 19-MAR-1993 (first entry)

XX 63 kD Cam PDE cDNA clone p12.3a from bovine brain.

XX Calcium/calmodulin; stimulated; cyclic; nucleotide;

XX phosphodiesterase; ss.

XX Bos taurus.

XX Key Location/Qualifiers

FT CDS 114..1715

FT /\*tag= a

XX W09218541-A1.

XX 29-OCT-1992.

XX 20-APR-1992; 92WO-US03222.

XX 19-APR-1991; 91US-0688356.

XX (UNIW ) UNIV WASHINGTON.

XX Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;

XX WPI: 1992-382051/46.

XX P-PSDB: AAR28404.

XX New DNA encoding mammalian cyclic nucleotide phosphodiesterase

XX - and derived vectors and host cells, useful for screening cpds.

XX for inhibitory or activating activity

XX Claim 7; Page 76; 133pp; English.

XX Oligonucleotide 63-1s, a fully redundant 23-mer was used to screen a

XX total bovine brain cDNA library in lambda ZAP II. A total of 21

XX putative positives were picked and rescreened with the probe from

XX plasmid p11.5B. One positive was obtd. designated p12.3a, which

XX codes for a protein sequence with most of the aligned peptides

XX isolated from bovine 63 kD Cam PDE.

XX See also AAQ30161-91.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 1844 BP; 417 A; 554 C; 511 G; 362 T; 0 other;

Query Match 43.4%; Score 1342.8; DB 13; Length 1844;

Best Local Similarity 90.4%; Pred. No. 0;

Matches 1470; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

QY 175 GCTGCGCTACATGCTGGAAGCAGTTGGAGATGGGAGATAAATGAGGAGCTGAAGAA 234

Db 224 GCTGCGCTACATGCTGGAAGCAGTTGGAGAACGGGAGGTAATGAGGAGCTGAAGAA 283

QY 235 AAATCTGGAGTACACAGCTTCTCTGCTGGAGCGGCTCTACATAGATGAGACACGGCAAT 294

Db 284 AAACCTGGAGTACACAGCTTCTCTGCTGGAGCGGCTCTATATAGATGAGACTCGGCAAT 343

QY 295 CTGGACACGGAGGACGAGCTGCGAGGAGCTGCGGTGAGATGCGCTTCGGAGGTGCG 354









[illegible]

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893  ACCAAGTCAGAAATGTGCATCGTGTACAATGATCGTTTCAGTGTGGAGAAATCACCACATC 952
1022 ACTCGGTCGTATCCAGGATATTCTGTATTAATGACAGATGTGTACTGGAGAAATCACCATTTA 1081
953  AGCTCTGTTTCCGATGATGATCAGAGATAGAG---ATGAACATTTTCATCAACCTCCAC 1009
1082  AGTCAGGCTTATCGCCTTCTCGAATGACGCGGAAATGATATTTGATTTAACTCTCA 1141
1010  AAGGATGAGTTGTAGAACTCCGAGCCCTGCTCATGTGAGATGGTGTGGCCACAGACATG 1069
1142  AAGGATGACTGGAGGAGTTTTCGAACCTTGTGAATTTGAATGGATGGTATGGCCACAGATATG 1201
1070  TCTGCGCAATTTCCAGCAAGTCGAGACCATGAAGACAGCCTTGTGCAACAGCTCGGAGAGGATT 1129
1202  TCTTGTACTTCCACAAATCAAGCAATGAAGACTGCTCTCGACAGCACCAGAGGCCAATT 1261
1130  ZACAAGCCCAAGGCCCTGTCTCTACTGTCTCATGCTGTGTACATCAGCCACCCCAACCAAG 1189
1262  GAAAGGCCAAAAGCCCTTATCCCTTATGCTGCATACAGCAGATATTAGCGATCCGACGAAT 1321
1190  CAGTGGTTGGTCCACAGCCGTTTGGACCAAGGCCCTCATGGAGAAATCTTCCGTGTCAGGT 1249
1322  GCATGGGACCTCCATCATCGCTGGACAATGTCACTCTGGAGAGATCTTCACAGAGGT 1381
1250  GACAAGGAGGACAGATGTGGCCCTGGCCCTTCTCCACTCTGTGTGACCGGCACTTCCACTCTA 1309
1382  GACAGAGAAGCAGAGCTGGGGCTGCTTTTCTCTCTGTGTGACCGAAAGTCCACTATG 1441
1310  GTGGCACAGTCTCAGATAGGTTGATCTGCACTCATTTGTCAGTGTGGAGCCCACTTCTGTGCTG 1369
1442  GTTCTCAGTGCACAGTGAAGTTTCATTTGATTTTCATCTGTGGAACCCACCTTCATCTGTGCTT 1501
1370  ACTGAGGTGCACAGAAAGATGTTTCAGCCCTCGCGGATGAGGACACTCCCAAGTCT 1423
1502  ACGGACATGACCGAGAAGATTTGTGAGTCCATTAAATCGATGAAACACTCTCAAACT 1555

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Search completed: August 10, 2003, 17:50:38  
Job time : 770 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2106.8	68.2	2265	2	US-08-940-332-1	Sequence 1, Appli
2	1347.6	43.6	1844	1	US-07-872-644-26	Sequence 26, Appl
3	1347.6	43.6	1844	1	US-08-297-494-26	Sequence 26, Appl
4	1347.6	43.6	1844	1	US-08-297-510-26	Sequence 26, Appl
5	1347.6	43.6	1844	1	US-08-479-532-26	Sequence 26, Appl
6	1347.6	43.6	1844	1	US-08-455-526-26	Sequence 26, Appl
7	1347.6	43.6	1844	1	US-08-455-525-26	Sequence 26, Appl
8	1347.6	43.6	1844	3	US-09-139-491-26	Sequence 26, Appl
9	1347.6	43.6	1844	3	US-09-139-491-26	Sequence 26, Appl
10	598	19.3	2693	5	PCR-US92-03222-26	Sequence 26, Appl
11	598	19.3	2693	1	US-07-872-644-50	Sequence 50, Appl
12	598	19.3	2693	1	US-08-297-494-50	Sequence 50, Appl
13	598	19.3	2693	1	US-08-297-510-50	Sequence 50, Appl
14	598	19.3	2693	1	US-08-479-532-50	Sequence 50, Appl
15	598	19.3	2693	1	US-08-455-526-50	Sequence 50, Appl
16	598	19.3	2693	1	US-08-455-525-50	Sequence 50, Appl
17	598	19.3	2693	5	PCR-US92-03222-50	Sequence 50, Appl
18	579.8	18.8	2656	1	US-07-872-644-16	Sequence 16, Appl
19	579.8	18.8	2656	1	US-08-297-494-16	Sequence 16, Appl
20	579.8	18.8	2656	1	US-08-297-510-16	Sequence 16, Appl
21	579.8	18.8	2656	1	US-08-479-532-16	Sequence 16, Appl
22	579.8	18.8	2656	1	US-08-455-526-16	Sequence 16, Appl
23	579.8	18.8	2656	1	US-08-455-525-16	Sequence 16, Appl
24	579.8	18.8	2656	3	US-09-139-491-16	Sequence 16, Appl
25	579.8	18.8	2656	3	US-09-139-491-16	Sequence 16, Appl
26	578.8	18.7	1625	5	PCR-US92-03222-16	Sequence 16, Appl
27	578.8	18.7	1625	1	US-07-872-644-48	Sequence 48, Appl
28	578.8	18.7	1625	1	US-08-297-494-48	Sequence 48, Appl

QY	175	GCTGGCTACATGTTGAACAGTTCGAGAAATGGGAGAGATAAATGAGGAGCTGAGAA	234
DB	148	GCTGGCTACATGTTGAACAGTTCGAGAAATGGGAGAGATAAATGAGGAGCTGAGAA	207
QY	235	AAATCTGGAGTACAGAGCTTCTGCTGGAAGCCGCTTACATAGATGAGACAGCGCAAT	294
DB	208	AAATCTGGAGTACAGAGCTTCTGCTGGAAGCCGCTTACATAGATGAGACAGCGCAAT	267
QY	295	CTTGACACGGAGGACAGCTGACAGAGCTGCGGTCAGATGCCGTGCCCTTCGGAGGTCG	354
DB	268	CTTGACACGGAGGACAGCTGACAGAGCTGCGGTCAGATGCCGTGCCCTTCGGAGGTCG	327
QY	355	GGAGTGGCTGGCCCTCCACCTTCAACACAGAGCCGCGGCCAAAGCCGCGAGCAGAGGA	414
DB	328	GGAGTGGCTGGCCCTCCACCTTCAACACAGAGCCGCGGCCAAAGCCGCGAGCAGAGGA	387
QY	415	GAAGCCCAAGTTCGGAACCATTTGTCACGCTGTGACAGCTGGGATCTTCGTGGAACGGAT	474
DB	388	GAAGCCCAAGTTCGGAACCATTTGTCACGCTGTGACAGCTGGGATCTTCGTGGAACGGAT	447
QY	475	GTTCGGAGAACATACACCTCTGTGGGCCCACTTACTTCTACTGCGGTTCTCAACTGTCT	534
DB	448	GTTCGGAGAACATACACCTCTGTGGGCCCACTTACTTCTACTGCGGTTCTCAACTGTCT	507
QY	535	CAAGAACCTGGATCTCTGCTGCTTTGATGTCTTTTCCCTTGAACAGGACGAGATGACCA	594
DB	508	CAAGAACCTGGATCTCTGCTGCTTTGATGTCTTTTCCCTTGAACAGGACGAGATGACCA	567
QY	595	TGCGCTGAGGACCATTTGTTTGTGATGCTGACTCGGCATTAACCTCATCAGCCGCTCAA	654
DB	568	TGCGCTGAGGACCATTTGTTTGTGATGCTGACTCGGCATTAACCTCATCAGCCGCTCAA	627
QY	655	GATTCGCCACTGTGTTTGTGATGTTCTGATGCTGAGAGAGCTATGGAAGTA	714
DB	628	GATTCGCCACTGTGTTTGTGATGTTCTGATGCTGAGAGAGCTATGGAAGTA	687
QY	715	CAAGAACTCTTACCAACACAGATCCACGACGCGATGTTTACCAGACAGTCATTCCTT	774
DB	688	CAAGAACTCTTACCAACACAGATCCACGACGCGATGTTTACCAGACAGTCATTCCTT	747
QY	775	CTTGCTCCGACAGGATGTTGCTGCTGCTGAGATTCAGCTGCTGCCATCATCTT	834
DB	748	CTTGCTCCGACAGGATGTTGCTGCTGCTGAGATTCAGCTGCTGCCATCATCTT	807
QY	835	TGCTGACGCTATCCATGATGATGACACAGCGGCACTACCAACAGCTTCCACATCCAGAC	894
DB	808	TGCTGACGCTATCCATGATGATGACACAGCGGCACTACCAACAGCTTCCACATCCAGAC	867
QY	895	CAAGTACAAATGTCGCTGCTGATGATGCTGCTGAGATTCACCAACATCCACATCAG	954
DB	868	CAAGTACAAATGTCGCTGCTGATGATGCTGCTGAGATTCACCAACATCCACATCAG	927
QY	955	CTCTGTTTCCGATGATGACAGGATGATGATGAACATTTTCATCAACCTCACCAAGGA	1014
DB	928	CTCTGTTTCCGATGATGACAGGATGATGATGAACATTTTCATCAACCTCACCAAGGA	987
QY	1015	TGAGTTTCTAGAACTCCGAGCCCTGGTCAATTGAGATGGTGGCCACAGACATGTCCTG	1074
DB	988	TGAGTTTCTAGAACTCCGAGCCCTGGTCAATTGAGATGGTGGCCACAGACATGTCCTG	1047
QY	1075	CAATTTCCAGCAAGTGAAGACCATGAAGACAGCCCTTGCAACAGCTGGAGAGGATTGACAA	1134
DB	1048	CAATTTCCAGCAAGTGAAGACCATGAAGACAGCCCTTGCAACAGCTGGAGAGGATTGACAA	1107
QY	1135	GCCCAAGGCCCTGTCTCTACTGCTCCATGCTGCTGACATCAGCCACCAACCAAGCAGTG	1194
DB	1108	GCCCAAGGCCCTGTCTCTACTGCTCCATGCTGCTGACATCAGCCACCAACCAAGCAGTG	1167
QY	1195	GTTCGTCCACAGCGTGTGGACCAAGGCCCTCATGAGGAATTTCTCCGTGAGGTTGACAA	1254
DB	1168	GTTCGTCCACAGCGTGTGGACCAAGGCCCTCATGAGGAATTTCTCCGTGAGGTTGACAA	1227

QY	1255	CGAGGCAGAGTTCGGGCTGCGCTTCTTCTCCATCTCTGTGACCGCACCTTCCACTCTAGTGGC	1314
DB	1228	CGAGGCAGAGTTCGGGCTGCGCTTCTTCTCCATCTCTGTGACCGCACCTTCCACTCTAGTGGC	1287
QY	1315	ACAGTCTCAGATAGGGTTCATCGACATTCATTTGGAGGCCACATTCCTCTGTGCTGACTGA	1374
DB	1288	ACAGTCTCAGATAGGGTTCATCGACATTCATTTGGAGGCCACATTCCTCTGTGCTGACTGA	1347
QY	1375	CGTGGCAGAGAGAGTGTTCAGGCCCTTGGCGGATGAGGACTCCAAAGTCTTAAAAACAGCC	1434
DB	1348	CGTGGCAGAGAGAGTGTTCAGGCCCTTGGCGGATGAGGACTCCAAAGTCTTAAAAACAGCC	1407
QY	1435	ACGCTTTTCACTGGCGCAGCCCTCTCTGGATGTGGAAGTGGGAGACCCCAACCCCTGATGT	1494
DB	1408	ACGCTTTTCACTGGCGCAGCCCTCTCTGGATGTGGAAGTGGGAGACCCCAACCCCTGATGT	1467
QY	1495	AGTCCAGCTTTTCTGTTCCACCTTGGGTCAAGCGCATTCAGGAGAAATGAACAGAAATGGAAGGA	1554
DB	1468	AGTCCAGCTTTTCTGTTCCACCTTGGGTCAAGCGCATTCAGGAGAAATGAACAGAAATGGAAGGA	1527
QY	1555	ACGGCAGCAAGTGGGATCACCAACAGATGTCATTGACGAGCTGTCCCCCTGTGAAGA	1614
DB	1528	ACGGCAGCAAGTGGGATCACCAACAGATGTCATTGACGAGCTGTCCCCCTGTGAAGA	1587
QY	1615	AGAGGCCCCCTCATCCCTGCGGAAGATGAACAAACAGAAATGGAATCTGATTTAGCC	1674
DB	1588	AGAGGCCCCCTCATCCCTGCGGAAGATGAACAAACAGAAATGGAATCTGATTTAGCC	1647
QY	1675	CTGGGCTGCGCCAGGCTTCTTATTGATGCCAAAGTGTTCATGATCATCAGCACCATCCAT	1734
DB	1648	CTGGGCTGCGCCAGGCTTCTTATTGATGCCAAAGTGTTCATGATCATCAGCACCATCCAT	1707
QY	1735	CAGGACTGCTCCCTCATCTGCTCCAGGAGCGTGTGCTGGAAGAAACAAACCCACCTG	1794
DB	1708	CAGGACTGCTCCCTCATCTGCTCCAGGAGCGTGTGCTGGAAGAAACAAACCCACCTG	1767
QY	1795	AAGCCAAATGCGCAGAGATTTGGGTGGGAAAGGCGCCCTCCACCTGACACCCACT	1854
DB	1768	AAGCCAAATGCGCAGAGATTTGGGTGGGAAAGGCGCCCTCCACCTGACACCCACT	1827
QY	1855	GGGTGCTGCTTAACTGTCGCGCAGCAAGCTGGGAACTTCAGGCTCCAGTGTGCT	1914
DB	1828	GGGTGCTGCTTAACTGTCGCGCAGCAAGCTGGGAACTTCAGGCTCCAGTGTGCT	1887
QY	1915	GTGCCATCCCTCAGGCTCTGGAATCTCTTCATGCGCAGGCTGCTGCCAGGAGCGGGA	1974
DB	1888	GTGCCATCCCTCAGGCTCTGGAATCTCTTCATGCGCAGGCTGCTGCCAGGAGCGGGA	1947
QY	1975	GCTTCTGAGGCTTCCAGGCGCTTGGGAAAGGTCAGAGATGCCAGCCCTGSGGACC	2034
DB	1948	GCTTCTGAGGCTTCCAGGCGCTTGGGAAAGGTCAGAGATGCCAGCCCTGSGGACC	2007
QY	2035	TCCCCCATCTTTTTCCTCCAAAGTTTCTAAGCAATACATTTTGGGGGTTCCTCAGCCC	2094
DB	2008	TCCCCCATCTTTTTCCTCCAAAGTTTCTAAGCAATACATTTTGGGGGTTCCTCAGCCC	2067
QY	2095	CCACCCAGATCTTAGCTGCGCAGGCTGCGGTGCCCTTTTCTCCCTGGGAGGCTG	2154
DB	2068	CCACCCAGATCTTAGCTGCGCAGGCTGCGGTGCCCTTTTCTCCCTGGGAGGCTG	2127
QY	2155	GAATAGGATAGAAAGCTGGGGTTTTCAGAGCCCTATGTTGGGAGGAGTGGATTC	2214
DB	2128	GAATAGGATAGAAAGCTGGGGTTTTCAGAGCCCTATGTTGGGAGGAGTGGATTC	2187
QY	2215	TTGAGGCTGCTGCTTCTTAGGATCTGGGAATGGGTGGGAGGACATCTCTTTCACC	2274
DB	2188	TTGAGGCTGCTGCTTCTTAGGATCTGGGAATGGGTGGGAGGACATCTCTTTCACC	2247
QY	2275	CCAGAAATGCGCTGCTTC	2292
DB	2246	CCAGAAATGCGGGAATTC	2265

## RESULT 2

US-07-872-644-26  
: Sequence 26, Application US/07872644  
: Patent No. 5389527  
: GENERAL INFORMATION:  
: APPLICANT: Beavo, Joseph A.  
: APPLICANT: Bentley, Kelley  
: APPLICANT: Charbonneau, Harry  
: APPLICANT: Sonnenburg, William K.  
: TITLE OF INVENTION: DNA Encoding Mammalian  
: TITLE OF INVENTION: Phosphodiesterases  
: NUMBER OF SEQUENCES: 58  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
: ADDRESSEE: Bicknell  
: STREET: Two First National Plaza, 20 South Clark  
: STREET: Street  
: CITY: Chicago  
: STATE: Illinois  
: COUNTRY: USA  
: ZIP: 60603  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/872,644  
: FILING DATE: 19920420  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/688,356  
: FILING DATE: 04-APR-1991  
: ATTORNEY/AGENT INFORMATION:  
: NAME: No. 5389527and, Greta E.  
: REGISTRATION NUMBER: 35,302  
: REFERENCE/DOCKET NUMBER: 27866/30822  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (312) 346-5750  
: TELEFAX: (312) 984-9740  
: TELEX: 25-3856  
: INFORMATION FOR SEQ ID NO: 26:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1844 base pairs  
: TYPE: NUCLEIC ACID  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 114..1715  
US-07-872-644-26

Query Match 43.6%; Score 1347.6; DB 1; Length 1844;

Best Local Similarity 90.6%; Pred. No. 0;

Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

Qy	175	GCTCGCTACATGCTGAAGCAGTTGGAGATGGGGATTAACATTGAGGAGCTGAAGAA	234
Db	224	GCTCGCTACATGCTGAAGCAGTTGGAGATGGGGATTAACATTGAGGAGCTGAAGAA	283
Qy	235	AAATCTGGAGTACACAGCTTCTGCTGGAAGCCGCTACATAGATGAGACACGGCAAT	294
Db	284	AAACCTGGAGTACACAGCTTCTGCTGGAAGCCGCTATATAGATGAGACTCGGCAAT	343
Qy	295	CTTGACACGAGGACGAGTGCAGAGCTGCGGTGATGCTGCTTGGAGGTGCG	354
Db	344	CCTGGACACGAGGATGAGTGCAGAGCTGCGGTGATGCTGCTTGGAGGTGCG	403
Qy	355	GGACTGCTGCTCCACCTTACCCAGCAGGCCCCGGCCAAAGCCCGCCGAGGAGGA	414
Db	404	GGACTGCTGCTCCACCTTACCCAGCAGGCCCCGGCCAAAGCCCGCCGAGGAGGA	460

Qy	415	GAAGCCCAAGTTCGAAAGCATTTGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAAACGGAT	474
Db	461	GAAGCCCAAGTTCGGAAGCATCGTGACGCGGTGCAGGCTGGCATCTTTGTGGAGCGAT	520
Qy	475	GTTCGGAGAACATACACCTCTGTGGGCCCCACCTTACTTACTCTGCTGGGTCTCACTACTGTCT	534
Db	521	GTTCGGAGAACATACACCTCTGTGGGCCCCACCTTACTTACTCTGCTGGGTCTCACTACTGTCT	580
Qy	535	CAAGAACCTGGATCTCTGGTCTTTGATGTCTTTTCTTGAACACGAGGACGAGATGACCA	594
Db	581	CAAGAACCTGGACCTTTGGTCTTTGATGTCTTTTCTTGAACCGGGGACGAGATGACCA	640
Qy	595	TGCCCTGAGGACCAATTTTGTGATGTCTGCTGACCTGGCATTAACCTCATCAAGCCCTTCAA	654
Db	641	CGCCCTGAGGACCAATCGTTTGTAGCTGTCTGCTGCGCACAACTCATCAAGCCCTTCAA	700
Qy	655	GATTCCTCCTGCTGTTTGTGATGTCTTCTGGATGCTTGGAGACAGGCTATGGGAAGTA	714
Db	701	GATTCCTCCTGCTGTTTGTGATGTCTTCTGGATGCTTGGAGACAGGCTATGGGAAGTA	760
Qy	715	CAAGAATCCTTACCACAAACAGATCCACGACGCGATGTTACCCAGACAGTCCATTTGCTT	774
Db	761	CAAGAACCTTACCACAAACAGATCCACGACGCTGACCTACCCAGAGGCTCCACTGCTT	820
Qy	775	CTTGCTCCGACAGGATGTGCTGCTGCTGCGAGATTGAGTCTCTGGCCATCATCTT	834
Db	821	CTTGCTCCGACAGGATGTGCTGCTGCTGCGAGATTGAGTCTCTGGCCATCATCTT	880
Qy	835	TGCTGACAGTATCCATGATGATGACACACGCGGACCTACCAACAGCTTCCACATCCAGAC	894
Db	881	TGCTGACAGTATCCATGATGATGACACACGCGGACCTACCAACAGCTTCCACATCCAGAC	940
Qy	895	CAAGTCAGATGTGCCATCGTGTACATGCTTACGTGCTGGAGATACCAACATCCAGATCAG	954
Db	941	CAATCGGATGCGCCATCTCTGTACACGCGCTCAGTGTGGAGATACCAACATCCAGATCAG	1000
Qy	955	CTCTGTTTCCGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1014
Db	1001	CTCGGTTTCCGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1060
Qy	1015	TGAGTTTGTAGAACTCCGAGCCCTGGTTCATTGAGATGGTGTGGCCACAGACATGCTCTG	1074
Db	1061	TGAGTTTGTAGAGCTCGGCGCTCTGGTTCATTGAGATGGTGTGGCCACAGACATGCTCTG	1120
Qy	1075	CCATTTCAGCAAGTGAAGACCATGAAGACAGCTTGAACAGCTGGAGAGATTGACAA	1134
Db	1121	CCATTTCAGCAAGTGAAGTCCATGAAGACAGCTTGAACAGCTGGAGAGATTGACAA	1180
Qy	1135	GCCCAAGGCCCTGCTCTACTGCTCCATGCTGCTGACATGACATGACATGACATGACATG	1194
Db	1181	GTCCAAGGCCCTCTCTGCTGCTTCTGCTGCTGACATGACATGACATGACATGACATG	1240
Qy	1195	GTTGGTCCACAGCGCTTGGACCAAGGCCCTCATGGAGGAATTTCTTCCGTAGGCTGACAA	1254
Db	1241	GTCGTTTCCACAGCGCTTGGACCAAGGCCCTCATGGAGGAATTTCTTCCGTAGGCTGACAA	1300
Qy	1255	GGAGCGAGTTGGCGCTGCGCTTCTCTCACTCTGTGACCGCACTTCCACTCTAGTGGC	1314
Db	1301	GGAGCGTGTGCTGGCGCTGCGCTTCTCTCACTCTGTGACCGCACTTCCACTCTAGTGGC	1360
Qy	1315	ACAGTCTCAGATAGGCTTTCATCGATTTCTTGTGGAGCCCACTTCTCTGCTGACTGA	1374
Db	1361	GCAGTCCAGATTTGTTTTCATCGATTTCTTGTGGAGCCCACTTCTCTGCTGACTGA	1420
Qy	1375	CGTGGCAGAGAGAGTGTTCAGCCCTTGGCGGATGAGGACTTCCAGTCTTAAACACAGCC	1434
Db	1421	TGTGGCTGAGAGAGTGTTCAGCCCTTGGCGGATGAGGACTTCCAGTCTTAAACACAGCC	1480
Qy	1435	CAGCTTTCAGTGGCGCGAGCCCTCTCTGATGTGAGTGGAGACCCCAACCTCTGATGT	1494
Db	1481	CAGCTTTCAGTGGCGCGAGCCCTCTCTGATGTGAGTGGAGACCCCAACCTCTGATGT	1540
Qy	1495	GGTCAGCTTTCGTTTCCACCTGGGTCAAGCGCATTCAGGAGAAATAGCAGAAATGGAAGGA	1554





1181 GTCCAAAGCCCTCTCTGCTGCTCATGCTGCTGACATCAGCCACCCCAAGCAGTG 1240  
1195 GTTGGTCCACAGCGGTGGACCAAGGCCCTCATGGAGGAATCTTCGCTAGGTGACAA 1254  
1241 GTCGGTTCACAGCGCTGGACCAAGGCCCTCATGGAGGAATCTTCGCGCCAGGTGACAA 1300  
1255 GGAGCGAGTGGGCGCTGCGCCCTTTTCFCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1314  
1301 GGAGGCTAGCTGGCGCTGCGCCCTTTTCFCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1360  
1315 ACAGTCTCAGATAGGTTTCATCGACTTCATTTGTGGAGCCCACTTCTCTGTGCTGACTGA 1374  
1361 GCAGTCCAGATAGTGTTCATCGACTTCATTTGTGGAGCCCACTTCTCTGTGCTGACTGA 1420  
1375 CGTGCAGAGAGAGTGTTCAGCCCTGCGCGGAGTGGAGCTTCCAGTCTTAAACCCAGCC 1434  
1421 TGTGCTGAGAGAGTGTTCAGCCCTGCGCGGAGTGGAGCTTCCAGTCTTAAACCCAGCC 1480  
1435 CAGCTTTCAGTGGCGCCAGCCCTCTCTGTGATGTGGAAGTGGAGCCCACTTCTGTGCT 1494  
1481 CAGCTTTCAGTGGCGCCAGCCCTCTCTGTGATGTGGAAGTGGAGCCCACTTCTGTGCT 1540  
1495 GGTGAGTTCGTTCCAGCTGGGTCAAGCGCATTCAGGAGATTAAGCAGAAATGAAGGA 1554  
1541 GGTGAGTTCGTTCCAGCTGGGTCAAGCGCATTCAGGAGATTAAGCAGAAATGAAGGA 1600  
1555 ACGGCGACAGTGGCATCACCAACAGCATTCATTCAGGAGTGTCCCTGTGAAGA 1614  
1601 ACGGCGGAGCGGCATCACCAACAGCATTCATTCAGGAGTGTCCCTGTGAAGA 1660  
1615 AGAGGCCGCCCATCCCTGCGGAGATGAACAAACAGAAATGGAAATCTGGATTAGCC 1674  
1661 AGAGGCCGCCCATCCCTGCGGAGATGAACAAACAGAAATGGAAATCTGGATTAGCC 1719  
1675 CTGGGCTGGCGCCAGGTCTTCATGAGTCCAAAGTGTGTTGATGATCAGCACCATCCAT 1734  
1720 --GGGGCTGGCGCCAGGTCTTCATGAGTCCAAAGTGTGTTGATGATCAGCACCATCCAT 1777  
1735 CAGGACTGGCTCCCGCATCTGCTCAAGGAGCGTG ---GTCGTGAAGAAACACCCAC 1791  
1778 CGGACTGGCTCCCGCATCTGCTCGAGGCGAATGGATGTCAAGGAACAGAAACCCAC 1837  
1792 CTGAAG 1797  
1838 CCGAAG 1843

RESULT 4  
US-08-297-510-26  
Sequence 26, Application US/08297510  
Patent No. 5602019

GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,510  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5602019and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1844 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 114..1715  
US-08-297-510-26

Query Match 43.6%; Score 1347.6; DB 1; Length 1844;  
Best Local Similarity 90.6%; Pred. No. 0;  
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;  
QY 175 GCTGGCTACATGTTGAAGCAGTGTGGAGAATGGGAGATTAACATTTGAGGAGCTCAAGAA 234  
Db 224 GCTGGCTACATGTTGAAGCAGTGTGGAGAATGGGAGGTTAAACATTTGAGGAGCTCAAGAA 283  
QY 235 AAATCTGGAGTACACAGCTTCTCTCTGCTGGAAGCCGTCTACATAGATGAGACACGGCAAT 294  
Db 284 AAACCTGGAGTACACAGCTTCTCTCTGCTGGAAGCCGTCTATATAGATGAGACTCGCAAT 343  
QY 295 CTTGACACGAGGAGGAGCTGCGAGAGCTGCGGTCAGATGCCGTGCTTTCGGAGGTGG 354  
Db 344 CTTGACACGAGGAGGAGCTGCGAGAGCTGCGGTCAGATGCCGTGCTTTCGGAGGTGG 403  
QY 355 GGACTGGCTGGCTCCACCTTCACCCAGCAGCCGGCCAAAGCCCGCAGCAGAGAGA 414  
Db 404 GGACTGGCTGGCTCCACCTTCACCCAGCAGCCGGCCAAAGCCCGCAG---CGAAGA 460  
QY 415 GAAGCCCAAGTTCGGAAGCATTTGTCACGCTGTGCAGGCTGGAGTCTTGTGGAAACGGAT 474  
Db 461 GAAGCCCAAGTTCGGAAGCATTTGTCACGCTGTGCAGGCTGGAGTCTTGTGGAGCGAT 520  
QY 475 GTTCGGGAGACATACACCTCTGTGGGCCCCACCTTACTCTACTGCGGTCTCAACTGTCT 534  
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QY 535 CAAGAACCTGGATCTCTGCTGCTTTGATGCTCTTTTCCCTTGAACACGAGCAGAGATGACCA 594  
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QY 595 TGCCCTGAGGACCATTTGTTTGTAGTGTGCTGACTCGGCATAACCTCATCAGCCGCTTCAA 654  
Db 641 CGCCCTGAGGACCATCGTTTTTGTAGTGTGCTGACTCGGCATAACCTCATCAGCCGCTTAA 700  
QY 655 GATTCCTGCTGTTTTTGTAGTGTGCTGATGCTTGGAGACAGGCTATGGGAAGTA 714  
Db 701 GATTCCTGCTGTTTTTGTAGTGTGCTGATGCTTGGAGACAGGCTATGGGAAGTA 760  
QY 715 CAAGAATCTTACCACCAACAGATCCAGCAGCCGATGTTACCCAGACAGAGCTTGTGTT 774  
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Db 821 CTGCTCCGACAGAGGATGGTCACTGCTGCGAGATGTAGGTCCTGGCCATCATCTT 880
Qy TGTGTCAGCTATCCATGATTATGAGCACACGGGCACTACCAACAGCTTCCACATCCAGC 894
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Db CAAATCGGAATGGCCATCCTGTACAACGACCGCTCAGTGTGGAGAAATCACCACATCAG 1000
Qy CTCTGTTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014
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Db TGAATTTGTAGAACCTCCAGGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1120
Qy CCATTTCCAGCAAGTGAAGACCATGAAGACAGCCCTTGAACAGCTGGAGAGATTGACAA 1134
Db CCATTTCCAGCAAGTGAAGTCCATGAAGACAGCCCTTGAAGAGCTGGAGAGATTGACAA 1180
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Db GGAGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1360
Qy ACAGTCTCAGATAGGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1374
Db GCAGTCCCAAGATGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420
Qy CTGGGCGAGAGAGAGTGTTCAGCCCTTGGCGGATGAGGACTCCCAAGTCTAAACACGCG 1434
Db TGTGCTGAGAGAGTGTTCAGCCCTTGGCGGATGAGGACTCCCAAGTCTAAACACGCG 1480
Qy CAGCTTTCAGTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1494
Db CAGCTTTCAGTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1540
Qy GCTCAGCTTCTGCTTCCAGCTGGTCAAGCGGATTCAGGAGATTAAGCAGAAATGGAAGGA 1554
Db GCTCAGCTTCTGCTTCCAGCTGGTCAAGCGGATTCAGGAGATTAAGCAGAAATGGAAGGA 1600
Qy ACGGCGAGAGTGGCATCACCAACAGATGCTCATGATGAGGAGTGTCCCTGCTGAGGA 1614
Db ACGGCGAGAGTGGCATCACCAACAGATGCTCATGATGAGGAGTGTCCCTGCTGAGGA 1660
Qy AGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1674
Db AGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1719
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Qy CAGGACTGGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1791
Db CAGGACTGGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1837
Qy CTGAAG 1797
Db CCGAAG 1843
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RESULT 5

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US-08-479-532-26
; Sequence 26, Application US/08479532
; Patent No. 5776752
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Blackwell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,532
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5776752and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ. ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1844 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 114..1715
; US-08-479-532-26
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Query Match 43.6%; Score 1347.6; DB 1; Length 1844;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

Qy 175 GTCGCGCTACATGCTGAAGCAGTTGGAGATGGGAGATAAATGAGAGCTGAAGAA 234
Db 224 GTCGCGCTACATGCTGAAGCAGTTGGAGAACGGGAGGTAACATTTGAGGAGCTGAAGAA 283
Qy 235 AAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTCATACATAGATGAGACGCGCAAT 294
Db 284 AAACCTGGAGTACACAGCTTCTCTGCTGGAGGCCGCTATATAGATGAGACTCGGCAAT 343
Qy 295 CTGGGACACGGAGGAGCTGCGAGGCTGCGGCTCAGATGCGGCTGCGGCTGCGGCTGCGG 354
Db 344 CTGGGACACGGAGGATGAGCTGCGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 403
Qy 355 GGAATGCTGGCTCCACCTTCCAGGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 414
Db 404 GGAATGCTGGCTCCACCTTCCAGGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 460
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QY 415 GAAGCCCAAGTTCGAAGCATTGTGCAGCTGTGTGAGGCTGGGATCTTCGTGGAACGGAT 474
Db 461 GAAGCCCAAGTTCGAAGCATTGTGCAGCTGTGTGAGGCTGGGATCTTCGTGGAACGGAT 520
QY 475 GTTCCGGAGAACATACACCTCTGTGGGGCCCACTTACTCTACTGGGGTTCACATGTCT 534
Db 521 GTTCCGGAGAACATACACCTCTGTGGGGCCCACTTACTCTACTGGGGTTCACATGTCT 580
QY 535 CAAGAACCTGATCTCTGGTCTTGTATGTCTTTTCCCTTGAACAGGCGAGATGACCA 594
Db 581 CAAGAACCTGATCTCTGGTCTTGTATGTCTTTTCCCTTGAACAGGCGAGATGACCA 640
QY 595 TGCCCTGAGGACCACTTGTGAGTGTCTGACTCGGCATAACCTCATCAGCGCGTTCAC 654
Db 641 CGCCCTGAGGACCACTTGTGAGTGTCTGACTCGGCACAACTCATCAGCGCGTTCAC 700
QY 655 GATTCCTCACTGTGTTTGTATGAGTTCCTGATGCTTGGAGAGAGCTATGGGAAGTA 714
Db 701 GATTCCTCACTGTGTTTGTATGAGTTCCTGATGCTTGGAGAGAGCTATGGGAAGTA 760
QY 715 CAAGAATCTTACCAACACAGATCCAGCGACCGATGTTACCCAGACAGTCCATGTCTT 774
Db 761 CAAGAATCTTACCAACACAGATCCAGCGACCGATGTTACCCAGACAGTCCATGTCTT 820
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QY 1075 CCATTTCCAGCAAGTGAAGACATGAAGACAGCCTTGAACAGCTGGAGAGATGACAA 1134
Db 1121 CCATTTCCAGCAAGTGAAGACATGAAGACAGCCTTGAACAGCTGGAGAGATGACAA 1180
QY 1135 GCGCAAGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
Db 1181 GCGCAAGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240
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QY 1255 GGAGGAGAGTGGGCGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1314
Db 1301 GGAGGAGAGTGGGCGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1360
QY 1315 ACAGTCTCAGATAGGTTTCATCGACTTCATTTGTGGAGCCCATCTCTCTGCTGCTGCTGCT 1374
Db 1361 ACAGTCTCAGATAGGTTTCATCGACTTCATTTGTGGAGCCCATCTCTCTGCTGCTGCTGCT 1420
QY 1375 CGTGCGAGAGAGTGTTCAGCCCTTGGCGGATGAGAGCTCCAGTCTTAAACACGCGC 1434
Db 1421 CGTGCGAGAGAGTGTTCAGCCCTTGGCGGATGAGAGCTCCAGTCTTAAACACGCGC 1480
QY 1435 CAGCTTTCAGTGGGCGGCGCTCTCTGATGATGGAAGTGGAGAGCCCAACCCCTGATGT 1494
Db 1481 CAGCTTTCAGTGGGCGGCGCTCTCTGATGATGGAAGTGGAGAGCCCAACCCCTGATGT 1540
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1495 GGTGAGCTTGTGTTCCAGCTGGTCAAGCGCATTCAGGAGATAAGCAGAAATGAAGA 1554  
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QY 1555 AGCGGACGAGTGGCATCACCAACGATGTCATTTGACGAGCTGTCCCTGTGAAGA 1614  
Db 1601 AGCGGACGAGTGGCATCACCAACGATGTCATTTGACGAGCTGTCCCTGTGAAGA 1660  
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Db 1661 AGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1719  
QY 1675 CTGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1734  
Db 1720 --GGGCGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1777  
QY 1735 CAGGAGCTGGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1791  
Db 1778 CAGGAGCTGGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1837  
QY 1792 CTGAAG 1797  
Db 1838 CCGAAG 1843

RESULT 6  
US-08-455-526-26  
; Sequence 26, Application US/08455526  
; Patent No. 5789553  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell,  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,526  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/297,494  
; FILING DATE: 29-AUG-1994  
; APPLICATION NUMBER: US 07/888,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5789553and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1844 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; ORIGIN: 114..1715  
; US-08-455-526-26

Query Match 43.6%; Score 1347.6; DB 1; Length 1844;  
Best Local Similarity 90.6%; Pred. No. 0;  
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

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224 GCTGCGCTACATGCTGAAGCAGTGGAGATGGGAGATAAATGAGAGCTGAAGAA 283  
225 GCTGCGCTACATGCTGAAGCAGTGGAGATGGGAGATAAATGAGAGCTGAAGAA 283  
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776 CTTGCTCCGACAGGAGTGGTGCATGCTGCTGCGGAGATGAGTCTCTGGCCATCAT 834  
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822 CTTGCTCCGACAGGAGTGGTGCATGCTGCTGCGGAGATGAGTCTCTGGCCATCAT 880  
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1496 (GCTCAGCTTTCGTTCCACCTGGCTCAAGCGCATTCAGGAGATAAAGCAAGATAAGGA 1554  
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1602 (ACGGCGGCGAGCGGCTCACCACAGATGCTCCATTTGAGAGCTGCTCCCTGCTGAGGA 1660  
1615 (AGAGGCGCGCGGCTCACCACAGATGCTCCATTTGAGAGCTGCTCCCTGCTGAGGA 1674  
1616 (AGAGGCGCGCGGCTCACCACAGATGCTCCATTTGAGAGCTGCTCCCTGCTGAGGA 1674  
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1779 (CGGACTGCTCCCGGCTCACCACAGATGCTCCATTTGAGAGCTGCTCCCTGCTGAGGA 1837  
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1793 CTGAAG 1797  
1838 CCGAAG 1843

RESULT 7  
US-08-455-525-26  
; Sequence 26, Application US/08455525  
; Patent No. 5800987  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESS: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,525

FILING DATE: 31-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/297,494

FILING DATE: 08/297,494

APPLICATION NUMBER: US 07/688,356

FILING DATE: 04-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: No. 5800987and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30822

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 1844 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 114..1715

US-08-455-525-26

Query Match 43.6%; Score 1347.6; DB 1; Length 1844;

Best Local Similarity 90.6%; Pred. No. 0;

Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

QY	715	CAAGAATCTTTACCAACACAGATCCACGACGCGGATGTTACCCAGACAGTCCATGCTT	774
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QY	835	TGCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCAACAGCTTCCACATCCAG	894
Db	881	TGCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCAACAGCTTCCACATCCAG	940
QY	895	CAAGTCAGATGTGCCATCGTGTACAATGATCGTGTGAGATGAGTCTCTGGCCATCATCTT	954
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QY	955	CTCTGTTTTCGATGATGAGGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAG	1014
Db	1001	CTCGGTTTTCGGAATGATGAGGATGAGGATGAGATGAGATGAGATGAGATGAGATGAG	1060
QY	1015	TGAGTTTCTAGAATCCGAGCCCTGCTCATTTGAGATGTTGTTGGCCACAGACATCTCTG	1074
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QY	1075	CCATTTCAGCAAGTGAAGACCATGAAGACAGCCCTTGAACAGCTGGAGAGATGACAA	1134
Db	1121	CCATTTCAGCAAGTGAAGTCCATGAAGACAGCCCTTGAACAGCTGGAGAGATGACAA	1180
QY	1135	GCCCAAGCCCTCTCTACTGCTCCATGCTGCTGATCATGACATCAGCCACCAACAGCAGTG	1194
Db	1181	GTCCAAGGCCCTCTCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1240
QY	1195	GTTGGTCCACAGCGTTGAGCAAGGCCCTCATGAGGAAATTTCTTCCTGAGGGTGAACA	1254
Db	1241	GTGCGTTTTCAGAGCCCTGGACCAAGGCCCTCATGAGGAAATTTCTTCCTGAGGGTGAACA	1300
QY	1255	GGAGGACAGATTGGGCTGCTGCTTCTTCTCCACTCTGTGACCCACTTCCACTCTAGTGC	1314
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QY	1315	ACAGTCTCAGATAGGTTTCATCGACTTCTGTTGGAGCCACATTTCTGTGCTGACATGA	1374
Db	1361	GCAGTCCAGATATGTTTTCATCGACTTCTGTTGGAGCCACATTTCTGTGCTGACATGA	1420
QY	1375	CGTGCACAGAGAGTGTTCAGCCCTCGCGATGAGGATCCCAAGTCTTAAACACAGCC	1434
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QY	1435	CAGCTTTTCAGTGGCCGCTGCTCTGATGTTGGAAGTGGAGACCCCAACCTGATGT	1494
Db	1481	CAGCTTTTCAGTGGCCGCTGCTCTGATGTTGGAAGTGGAGACCCCAACCTGATGT	1540
QY	1495	GGTCACTTTCTGTTCCACTGCTGCTCAAGCGATTCAGGAGATTAAGCAGAAATGAAGA	1554
Db	1541	GGTCACTTTCTGTTCCACTGCTGCTCAAGCGATTCAGGAGATTAAGCAGAAATGAAGA	1600
QY	1555	ACGGCACAGTGTGATCACCACACAGATGTCATTTGACGAGTGTCCCTCTGTAAGA	1614
Db	1601	ACGGCACAGTGTGATCACCACACAGATGTCATTTGACGAGTGTCCCTCTGTAAGA	1660
QY	1615	AGAGGCCCTCCATCCCTGCGGAGATGAACACACAGATGGAATCTGGATAGCC	1674
Db	1661	AGAGGCCCTCCATCCCTGCGGAGATGAACACACAGATGGAATCTGGATAGCC	1719
QY	1675	CTGGGCTGGCCAGGTTCTTATGAGTCCAAAGTGTGTTGATGTCATCAGCACCATCAT	1734
Db	1720	--GGGGCTGGCCAGGTTCTTATGAGTCCAAAGTGTGTTGATGTCATCAGCACCATCAT	1777
QY	1735	CAGGACTGGCTCCCTCATCTGCTCAAGGGAGCGTG--GTCGTGGAAGAACACCCAC	1791
Db	1778	CGGGAAGTGGCTCCCTCATCTGCTCGAGGGGGAATGGATGTCAAGGAACAGAAACCCAC	1837
QY	1792	CTGAAG	1797

Page 10

Page 10

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Qy 1435 CAGCTTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGAGACCCCAACCCCTGATG 1494  
Db 1481 CAGCTTCCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGAGACCCCAACCCCTGACGT 1540  
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Db 1541 GGTGAGCTTCCGCTCCACCTGGACCAATATCATTCAGGAGAAACAGCAGAAATGGAAGGA 1600  
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RESULT 9

PCT-US92-03222-26  
; Sequence 26, Application PC/TUS9203222  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/03222  
; FILING DATE: 19920420  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Noland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1844 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 114..1715  
; PCT-US92-03222-26  
  
Query Match 43.6%; Score 1347.6; DB 5; Length 1844;  
Best Local Similarity 90.6%; Pred. No. 0;  
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;  
  
Qy 175 GCTCGCTACATGCTGAAGCAGTTGGAGATGGGAGATAAACAATTCAGGAGCTGAAGAA 234  
Db 224 GCTCGCTACATGCTGAAGCAGTTGGAGATGGGAGATAAACAATTCAGGAGCTGAAGAA 283  
Qy 235 AAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTCTACATAGATGAGACACGCAAT 294  
Db 284 AAACCTGGAGTACACAGCTTCTCTGCTGGAGCCGCTCTATATAGATGAGACTCGCAAT 343  
Qy 295 CTTGGACACGGAGGACGAGCTGCGAGAGCTGCGGTTCAGATGCCGTCTTCGGAGGTGCG 354  
Db 344 CTTGGACACGGAGGATGAGCTGCGAGAGCTGCGGTCTGATCGGTGCTTCAGAGGTGCG 403  
Qy 355 GGACTGGCTGGCTCCACCTTCACCCAGCAGCCCGGGCCAAAGCCCGCCAGCAGGAGA 414  
Db 404 GGACTGGCTGGCTCCACCTTCACCCAGCAGCCCGGGCCAAAGCCCGAG---CGAAGA 460  
Qy 415 GAAGCCCAAGTTCCGAAGCATTGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAAACGAT 474  
Db 461 GAAGCCCAAGTTCCGAAGCATTGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAGCGAT 520  
Qy 475 GTTCCGGAGAACATACACCTCTGTGGGCCCCACCTTACTCTCTCGGTTCCTCAACTGTCT 534  
Db 521 GTTCCGGAGAACATACACCTCTGTGGGCCCCACCTTACTCTCTCGGTTCCTCAACTGTCT 580  
Qy 535 CAAGAACCTGGATCTCTGGTGTCTTGTATGCTCTTCTTCCCTTGAACAGCAGCAGCAGATGACCA 594  
Db 581 CAAGAACCTGGATCTCTGGTGTCTTGTATGCTCTTCTTCCCTTGAACAGCAGCAGCAGATGACCA 640  
Qy 595 TGCCCTGAGGACCACTTGTCTTGTAGTGTCTGACTCGGCATACCTCTCATCAGCCCTCAAA 654  
Db 641 CGCCCTGAGGACCACTTGTCTTGTAGTGTCTGACTCGGCATACCTCTCATCAGCCCTTAA 700  
Qy 655 GATTCCCACTGTGTTTGTATGAGTGTCTTCCGTGGCTTGGAGACAGCTATGGGAAGTA 714  
Db 701 GATTCCCACTGTGTTTGTATGAGTGTCTTCCGTGGCTTGGAGACAGCTATGGGAAGTA 760  
Qy 715 CAAGAATCCTTACCACAAACAGATCCAGCAGCCGATGTTTACCAGACAGTCCCATTCGTT 774  
Db 761 CAAGAATCCTTACCACAAACAGATCCAGCAGCCGATGTTTACCAGACAGTCCCATTCGTT 820  
Qy 775 CTTGCTCCGACAGGATGTGTCACCTGCTCGGAGATTGAGTCTCTGGCCATCATCTT 834  
Db 821 CTTGCTCCGACAGGATGTGTCACCTGCTCGGAGATTGAGTCTCTGGCCATCATCTT 880  
Qy 835 TGCTGACGCTATCCATGATTATGAGCAGCAGGCGACTTACCACAGCTTCCACATCCAGAC 894  
Db 881 TGCTGACGCTATCCATGATTATGAGCAGCAGGCGACTTACCACAGCTTCCACATCCAGAC 940  
Qy 895 CAAGTCAGATGTGCCATCGTGTACATGATGCTGTCTAGTGTGGAGAAATCACCACATCAG 954  
Db 941 CAATCGGAATGCGCCATCTCTGTACAAACGACCCGCTAGTGTGGAGAAATCACCACATCAG 1000  
Qy 955 CTCTGTTTCCGATTGATGAGATGATGATCAACATTTTTCATCAACCTCACAAGGA 1014  
Db 1001 CTCTGTTTCCGATTGATGAGATGATGATCAACATTTTTCATCAACCTCACAAGGA 1060  
Qy 1015 TGAGTTTGTAGAACTCCGAGCCCTGGTTCATTGAGATGTTTGGCCACAGACATGTCTG 1074





Db 782 AAGATCCCAATTTCTGCACTTGTCTCTATTTCTGAGGCGCTTGAAGTGGGATACAGCAAG 841  
Qy 713 TACAGAGATCCTTACCAACACAGATCCACGCGCGATGTACCCAGACAGTCCATTGC 772  
Db 842 CACAAAATCCTTACCATAAGTACGACCTCGCATGTATACAGACAGTGCATTAC 901  
Qy 773 TTTCTGTCTCCACAGGAGTGGTGCACCTGCTGCGAGATTTGAGCTCCTGGCCATCATC 832  
Db 902 CTCCTCTATAGACAGAGTGGCGACTGCTGACGAGCTGGAGATCTTTGCTATATC 961  
Qy 833 TTTGCTGAGTATCCATGATATGAGACACGCGGACTACCAACAGTTCACATCCAG 892  
Db 962 TTTCTAGTGCATCCATGATAGTACGACATACCGGAACCAACAAATTTCCACATTCAG 1021  
Qy 893 ACCAAGTCAGATGTCATGCTGACAAATGATGCTGAGCTGCGGAGTACCAACATC 952  
Db 1022 ACTGGTGTATCCAGCTATTTCTGTATATGACAGATCTGTACTGGAGATACCAATTA 1081  
Qy 953 AGCTCTGTTTCCGATTTGATGAGGATGATGAG---ATGAACATTTTTCATCAACCTCAC 1009  
Db 1082 AGTCAGCTTATCCCTTCTGCAAGATGACGAGGAATGATATTTGATTAACCTCTCA 1141  
Qy 1010 AAGATGAGTTTGTAGAACTCCGAGCCCTGTCTATGATGATGTTGGCCACAGACATG 1069  
Db 1142 AAGGATGACTGGAGGAGTTTTCGAACCTTGTGTAATTTGAAATGTTGATGGCCACAGATG 1201  
Qy 1070 TCCTGCGCATTTCCAGCAAGTGAAGACCATGAGACGCTTGCACAGCTGGAGGATT 1129  
Db 1202 TCTTGTCACTTCCAAACAAATCAAGCAATGAAGACTGCTGTGACGAGCCAGAACCAAT 1261  
Qy 1130 GACAAGCCCAAGGCGCTTCTCTACTGCTCATGCTGTGACATCAGCCACCCCAACCAAG 1189  
Db 1262 GAAAAGCCAAAGCCTTATCCCTTATGCTGATACAGCAGATATAGCCATCCAGCAAA 1321  
Qy 1190 CAGTGGTTTGTCCACAGCCGTTGGACCAAGCCCTCATGAGGAAATTTCCCTCAGGGT 1249  
Db 1322 GCATGGGACCTTCCATCATCGTGGACAAATGTCATCTCTGGAGGATTTCTTCAGACAGGGT 1381  
Qy 1250 GACAAGGAGGAGAGTGGGCGCTCCCTTTCTCCACTCTGTGACCGCACCTTCACACTCA 1309  
Db 1382 GACAGAGAGAGAGTGGGCGCTCCCTTTCTCTCTGCTGTGACCGGAACTCCACTATG 1441  
Qy 1310 GTGCAAGTCTCAGATAGGTTTTCATGACTTATTTGGAGCCCACTTCTGTGCTG 1369  
Db 1442 GTTGCTCAGTACCAAGTAGGTTTCATTGATTTTCATGTTGGAACCCACCTTCACCTGTGCT 1501  
Qy 1370 ACTGAGTGGCAGAGAGAGTGTTCAGCCCTGGCGGATGAGGACTCCAACT 1423  
Db 1502 ACGGACATGACCGAGAGATTTGTAGTCCATTAATCGATGAAGCACTCTCAAACT 1555

RESULT 11

US-08-297-494-50  
; Sequence 50, Application US/08297494  
; Patent No. 5580771  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,494  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 558077land, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2693 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 176..2077  
US-08-297-494-50  
Query Match 19.3%; Score 598; DB 1; Length 2693;  
Best Local Similarity 67.9%; Pred. No. 2.4e-154;  
Matches 851; Conservative 0; Mismatches 400; Indels 3; Gaps 1;  
Qy 173 AGCTGCGCTACATGGTGAAGCAGTTGGAGAAATGGGGAGATAAACAATTGAGGAGCTGAAG 232  
Db 302 AGATTACGGTCTTTGGTCAACAATTAGAGAGAGGGGAAGCTTCAGTGTAGATCTTTAAG 361  
Qy 233 AAAAATCTGGAGTACACAGCTTCTCTGCTGGAGCCGCTCATATAGATGAGACAGCGCAA 292  
Db 362 AAGAATTTGGAATATGACGCCACAGTGTCTTGAATCTGTGTATTTATGATGAACAAGGAGA 421  
Qy 293 ATCTTTGACACGAGGAGCAGCTGCAGGAGCTGCGGTGAGTGCCTTCGAGAGGTG 352  
Db 422 CTCCTGGATACAGAGGATGAGCTCAGTCACTCAGTCACTGCTGCTCTCTGAGGTC 481  
Qy 353 CGGAGCTGGCTGGCTTCCACCTTCCACGAGGAGCCGCGCCAAAGGCCGCGGACAG 412  
Db 482 CGAGACTGGCTGGCTCCACCTTCCACGCGGAGATGGGGATGATGCTCAGGAGGAGCGAC 541  
Qy 413 GAGAAGCCCAAGTTCCGAAGCATTGTGCACGCTGTGACGCTGGGATCTTCTGGAACGG 472  
Db 542 GAGAAGCCCGGTTCAAGAGCATCGTTCCACGAGTGGAGGCTGGGATATTTGAGGAGA 601  
Qy 473 ATGTTCCGGAACATACACCTCTGTGGGCCCCACTTACTCTACTGCGGTCTCAACTGT 532  
Db 602 ATGATAGACGACATCAACATGTTGATGATGAGCTATCCACAGCTGTTATTGAGGCA 661  
Qy 533 CTCAAGACCTGGATCTCTGGTGTGTTGATGTCTTTTCTTTTGAACACGAGCAGCAGATGAC 592  
Db 662 TTAAGGATGTGGCAAGTGGTCTTTTCCACGCTCTTTTCCCTCAATGAGGCCAGTGGGAT 721  
Qy 593 CATGCCCTGAGGACCATTTGTTTGTGATGTTGCTGACTCGGCATTAACCTCATCAGCGGCTTC 652  
Db 722 CATGACCTGAAATTTATTTTCTATGAACACTACTACACGTTATGATCTGATCAGCGGTTTC 781  
Qy 653 AAGATCCCACTGTTGTTTGTGATGTTTCTGATGCTTGGATGCTTGGAGACAGGCTATTGGGAAG 712  
Db 782 AAGATCCCACTTTCGCACTTGTCTCATTTTGGAGGCCCTTGGAGTGGGATGAGCAG 841  
Qy 713 TACAAGATCCTTACCAACACAGATCCACGCGGATGTTTACCCAGACAGTCCATTGC 772

Db 842 CACAAAAATCCTTACCATAAATTAATGACGCTGCCGATGTTACACAGACAGTGCCATTAC 901  
QY 773 TTCTTCTCGCCGACAGGAGTGTGCATGCTGCTCGGAGATTGAGCTCTGTGCCCATCATC 832  
Db 902 CTCCTCTTAAGACAGGAGTGTGCGAACTGGCTGACGGAGTGGAGATCTTTGCTATAATC 961  
QY 833 TTTGCTGAGCTATCCATGATTATGACACAGCGGCACTACCAACAGCTTCCACATCCAG 892  
Db 962 TTCTCAGCTGCCATCCATGACTACGAGCATACCGGAACCAACCAAAATTTCCACATTCAG 1021  
QY 893 ACCAAGTACAGATGCGCATCTGTACATGATGCTTGTAGTCTGTGAGAAATCACCACATC 952  
Db 1022 ATCGCTGTATCCAGCTATCTGTATATGACATCTGTACTGGAGAAATCCCATTTA 1081  
QY 953 AGCTCTGTTTCCGATGTATGACGAGTATGAG---ATGCAATTTTCATCAACCTCAC 1009  
Db 1082 ATGCGAGCTTATCGGCTTCTGCAAGATGACGAGGAATGAATATTTGATTAACCTCTCA 1141  
QY 1010 AAGATGAGTGTGTAGAACTCCGAGCCCTGCTCATTTGATGATGTTGTCGCCACAGCATG 1069  
Db 1142 AAGATGAGTGTGAGGAGGTTTTCGAACCTTGGTAATGTAATGTTGATGCCACAGATATG 1201  
QY 1070 TCTTCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGCACACAGCTGGAGAGGATT 1129  
Db 1202 TCTTGTCTATCCAAATCAAGCAATGAGACTGTCTGACGAGCCAGAGCCATT 1261  
QY 1130 GACAAAGCCCAAGCCCTGTCTACTGCTTCCATGCTGATGATGATGATGATGATGATGATG 1189  
Db 1262 GAAAGCCCAAGAGCCCTTATCCCTTATGCTGATACAGCAGATATTAAGCCATCCAGCAAAA 1321  
QY 1190 CAGTGTGTTGTCACAGCGCTGTGACCAAGGCGCTCATGAGGAAATTTCTCGTCAGGTT 1249  
Db 1322 GCATGGGACCTCCATCATCGCTGGACAAATGTCACTCTCTGGAGGATTTCTCAGACAGGT 1381  
QY 1250 GACAGGAGGAGAGTGTGGCTGCTGCTTCTTCCACTCTGTGACGCTTCCACTCTCA 1309  
Db 1382 GACAGAGAGAGAGCTGGGCTGCTTTTCTCTCTGTGTGACGAGAAAGTCCACTATG 1441  
QY 1310 GTGGACAGCTCAGATAGGTTTCACTGATGATGATGATGATGATGATGATGATGATGATG 1369  
Db 1442 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1501  
QY 1370 ACTGAGTGGGAGAGAGTGTTCAGCCCTTGGCGGATGAGGACTCCAAAGTCT 1423  
Db 1502 ACGGACATGACGGAAGATTGTGAGTCCATTAATCGATGAACCTCTCAAACT 1555

## RESULT 12

US-08-297-510-50  
; Sequence 50, Application US/08297510  
; Patent No. 5602019

## GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases

## NUMBER OF SEQUENCES: 58

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/297,510  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5602019and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/POCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2693 base pairs  
; TYPE: nucleic acid  
; STRANDELNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; NAME/KEY: CDS  
; LOCATION: 176..2077  
US-08-297-510-50

Query Match 19.3%; Score 598; DB 1; Length 2693;  
Best Local Similarity 67.9%; Pred. No. 2.4e-154;  
Matches 851; Conservative 0; Mismatches 400; Indels 3; Gaps 1;

QY 173 AGGCTGGCTACATGTAAGCAGTGTGGAGATGGGAGATAAACAATTGAGGAGCTGAAG 232  
Db 302 AGATTACGCTCTTTGGTCAACAATAGAGAGAGGAGGAGCTTCACTGGTATCTTAAG 361  
QY 233 AAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTACATAGATGACACAGCGCA 292  
Db 362 AGATTGGAATATGACGACAGTGTGGAATCTGTGTATATGATGAAACAGGAGA 421  
QY 293 ATCTTGACACGAGGAGAGCTGACAGAGTGGGCTGAGATGCGGCTGCTTCGAGGAGTG 352  
Db 422 CTCCTGATACAGAGGATGAGCTCAGTACATTCAGTACAGTGTGCTGCTTCTGAGGTC 481  
QY 353 CGGACTGGCTGGCTCCACCTTCCACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 412  
Db 482 CGAGACTGGCTGGCTCCACCTTCCACGCGGAGATGGGAGATGATGCTCAGAGAGGAGG 541  
QY 413 GAGAGCCCAAGTTCGGAAGCATTTGTCAGCTGTGAGGCTGGGATCTTCGTGGAACGG 472  
Db 542 GAGAGCCCGGTTCAAGAGCATCGTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 601  
QY 473 ATGTTCCGAGAGACATACACCTCTGTGGGCGCCACTTACTCTACTCTGCTGCTCAACTGT 532  
Db 602 ATGTATAGCGGACATCAACATGTTGGAGTGTGAGCTATCCACAGCTGTATTGAGGCA 661  
QY 533 CTCAAGAACCTGGATCTCTGCTGCTTTGATGCTTTTCTTGAACAGGAGGAGGAGGAGGAG 592  
Db 662 TTAAGGATGTGGACAAGTGTCTCTTTGAGCTCTTTTCCCTCAATGAGGAGGAGGAGGAG 721  
QY 593 CATGCCCTGAGGACATTTGTTTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652  
Db 722 CATCACTGAAATTTATTTCTATGAACTACTACAGCTTATGATCTGATCAGCCGTTTC 781  
QY 653 PAGATTCGACATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 712  
Db 782 PAGATTCGACATGTTGCTCAITTTGTGGGCGCCCTGGAGTGGGATGATGATGATGATGATG 841  
QY 713 TACAAGATCTTACCAACACAGATCCAGAGCCGATGTTACCCACAGCTGATTCG 772  
Db 842 CACAAAATCTCTACCACTTAATGACAGCTGCCGATGTTACAGAGAGAGCTCATATAC 901  
QY 773 TCTTGTCTCCGACAGAGGATGGTGCATGCTGTGCGAGATGAGCTCTCTGGCCATCATC 832

Db 902 CTCCTCTATAAGACAGAGGAGTGGCGAACTGGCTGACGGAGCTGGAGATCTTTGCTATAATC 961  
QY 833 TTTGCTGAGCTATCATGATTATGAGCACAGCGGCACTACCAACAGCTTCCACATCCAG 892  
Db 962 TTTGCTGAGCTATCATGATTATGAGCACAGCGGCACTACCAACAGCTTCCACATCCAG 1021  
QY 893 ACCAAGTCAAGATGTGCGCATCGTGTACAAATGATCTTCAGTGTGCGAAGTCAACACATC 952  
Db 1022 ACTCGTCTGATCCAGCTATCTGTATATGACAGATCTGTACTGGAGATCAACATTA 1081  
QY 953 AGCTCTGTTTCCGATGATGACAGGATGATGAG---ATGACATTTTCAACACCTCACC 1009  
Db 1082 AGTGAGCTTATCGCTTCTGCAAGATGACGAGGAATGAATATTTGATTAACCTCTCA 1141  
QY 1010 AAGGATGAGTTGTAGAACTCCGAGCCTGCTGATGAGTGGTGTGGCCACACATG 1069  
Db 1142 AAGGATGAGTTGTAGAACTCCGAGCCTGCTGATGAGTGGTGTGGCCACACATG 1201  
QY 1070 TCCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGAACAGCTGGAGAGATT 1129  
Db 1202 TCTTGTCACTTCCAAACAATCAAGCAATGAAGACTGCTCTGCACGACCCAGAGCCATT 1261  
QY 1130 GACAAAGCCAAAGCCCTCTCTACTGCTCAATGCTGTGACATCAGCAACCCAAAG 1189  
Db 1262 GAAAGCCAAAGCCCTTATCCCTTATGCTGTGATACAGCAGATATTAGCCATCCAGCAAAA 1321  
QY 1190 CAGTGTGTTGTCACAGCGCTTGGACCAAGCCCTCATGAGGAATCTTCGTCAGGTT 1249  
Db 1322 GCATGGGACCTCCATCATCGTGGACAATGATCATCTCTGGAGAGATTCTTCAGACAGGT 1381  
QY 1250 GACAAAGGAGGAGCTGGGCTGCTCTTCTTCCACTGTGTGACCGCACTTCCACTCTA 1309  
Db 1382 GACAGAGAAGCAGAGCTGGGCTGCTCTTCTCTCTGTGTGACCGAAAGTCCACTATG 1441  
QY 1310 GTGGCACAGTCTCAGATAGGTTTCACTGCTCACTTCACTGTGGAGCCACATTTCTGTGTG 1369  
Db 1442 GTTGTCTGCTCACAAAGTAGGTTTCACTGCTGATTTTCACTGTGGAAACCCACTTCACTGTGTT 1501  
QY 1370 ACTGAGCTGGCAGAGAAGAGTGTTCAGGCCCTTGGCGGATGAGGACTTCCAAAGTCT 1423  
Db 1502 ACGGACATGACCGAGAAGATGTGAGTCCATTAATCGATGAACCTCTCAAACT 1555

RESULT 13

; Sequence 50, Application US/08479532  
; Patent No. 5776752

; GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESS: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,532  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/297,494  
; FILING DATE:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5776752and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2693 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 176..2077  
; US-08-479-532-50

Query Match

Best Local Similarity 19.3%; Score 598; DB 1; Length 2693;  
Matches 851; Conservative 0; Mismatches 400; Indels 3; Gaps 1;

QY 173 AGGCTGCCCTACATGGTGAAGCAGTTGGAGATGGGAGATAAACATTTGAGGAGCTGAAG 232  
Db 302 AGATTACGCTCTTTGGTCAACAATTAGAGAGAGGGGAAGCTTCAGTGTGTAGTCTTAAG 361  
QY 233 AAAAATCTGGAGTACACAGCTTCTGCTGGAAGCCGCTACATAGATGAGACACGGCAA 292  
Db 362 AAGAATTTGGAATATGCAGCCACAGCTGTGAATCTGTGTATTTATGATGATAAACAAGAGA 421  
QY 293 ATCTTGGACACGAGCAGCAGCTGCGGTACAGTGCCTGCTGCTGCTGCTGCTGCTGCTG 352  
Db 422 CTCCTGGATACAGAGGATGAGCTCAGTGACATTCAGTGTGCTGCTGCTGCTGCTGCTG 481  
QY 353 CGGAGCTGGCTGCCCTCCACCTTACCCACAGAGCCGCGGCAAGCCGCGCAGCAGAG 412  
Db 482 CGAGACTGGCTGGCTCCACCTTACCGCGCAGATGGGATGATGCTCAGAGAGAGCGAC 541  
QY 413 GAGAAGCCCAAGTTCGGAAGCATTTGACAGCTGTGACGCTGTCAGGCTGGGATCTTCGTGGAACG 472  
Db 542 GAGAAGCCCGGTTCAAGAGCATGTTACCGCAGTGCAGGCTGGGATATTTGTGGAGAGA 601  
QY 473 ATGTTCCGGAGAACATACACCTTCTGTGGGCCCCACTTACTCTACTCTGCTGCTGCTGCT 532  
Db 602 ATGTATAGAGCAGCATCAACATGTTGGACTGAGCTATCCACCAGCTGTTATTGAGGCA 661  
QY 533 CTCGAAGAACCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592  
Db 662 TTAAGAGGATGTGCAAGTGGTCTTTGACGCTTTTCCCTCAATGAGGCCAGTGGGAT 721  
QY 593 CATGCCCTGAGGACCATTTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652  
Db 722 CATGCATGAAATTTATTTTCTATGAACCTACTCACACGTTATGATCTGTATGATGATG 781  
QY 653 AAGATTCACCTGTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 712  
Db 782 AAGATTCACCTTTCTGCACTTCTGCTATTTTGGAGGCCCTGGAAGTGGGATACAGCAAG 841  
QY 713 TACAAGAAATCTTACCAACAACAGATCCACGAGCGGATGTTTACCCAGACAGTCCATTCG 772  
Db 842 CACAAAATCTTACCATTAATTAATGACAGCTGCGGATGTTTACACAGACAGTGCATTAC 901  
QY 773 TTTCTGCTCCGACAGGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 832  
Db 902 CTCCTCTATAAGACAGGAGTGGCGAACTGGCTGACGAGCTGGAGATCTTTGCTATAATC 961

833 TTGCTGACGCTATCATGATGATGAGCACAGGCGACCTACCAACAGCTTCCACATCCAG 892  
Db TTCTCAGCTGCCATCCATGACTAGGACATACCGGAACCAACCAATTTCCACATTCAG 1021  
893 ACCAAGTCAAGTGTGCCATCTGTACATGATCTGAGTGTGAGGATCACCACATC 952  
Db ACTCGGTGATCCAGCTATCTGTATATGAGAGATCTGTGATGAGATCACCATTTA 1081  
895 AGCTCTGTTTCCGATGTAGTGAAGATGATGAG ---ATGAACATTTTTCATCAACCTCAC 1009  
Db AGTGACGCTTATCGCTTCTGCAAGATGAGGAGAAATGAATTTTGAATTAACCTCTCA 1141  
1010 AAGGATGAGTTGTAGAACTCCGAGCCCTGGTCAATTGAGATGGTGTGGCCACAGCATG 1069  
Db AAGGATGAGTGGAGGAGTTTGAACCTTGGTAATTTGAAATGGTGTGATGCCACAGATG 1201  
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Db GAAAAGCCAAAGCCCTTATCCCTTATGCTGCTGATACAGCAGATATTAGCCATCCAGCAAA 1321  
1190 CAGTGTGTGCTCAGACAGCGTGTGAGCAAGGCCCTCATGGAGGAATTTCTCGTCAAGGT 1249  
Db GCATGGGACCTCATCATGCTGGAATGTCTACTCTGAGGAGTCTTTCAGACAGGCT 1381  
1250 GACAAGGAGGACAGATGGGCTGCTCTTCTCCACTCTGTGACCGCACTTCCACTCTA 1309  
Db GACAGAGAAGCAGAGCTGGGCTGCTCTTCTCTGCTGTGACCAAGTCCACTATG 1441  
1310 GTGGCAGCTCAGATGAGTGTATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1369  
Db GTGCTCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1501  
1370 ACTGAGCTGGCAGAGAGAGTGTTCAGCCCTGGCGGATGAGACTCCAACTCT 1423  
Db ACAGCATACCGCAGAGATGTGAGTCCATTAATCGATGAACCTCTCAAACT 1555

RESULT 14  
US-08-455-526-50  
Sequence 50, Application US/08455526  
Patent No. 5789553  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,526  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/297,494

FILING DATE: 29-AUG-1994  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5789553and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2693 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 176..2077  
US-08-455-526-50

Query Match 19.3%; Score 598; DB 1; Length 2693;  
Best Local Similarity 67.9%; Pred. No. 2.4e-154;  
Matches 851; Conservative 0; Mismatches 400; Indels 3; Gaps 1;

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QY 293 ATCTTTGACACAGGAGGAGCTGACAGGAGTGCAGATGCGGTCAGATGCGCTTCGAGG 352  
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Db 842 CACAAAATCTTACCATATTAATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901  
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Db 902 CTCCTCTATAAGACAGGAGTGGGAACTGGCTGAGCGGAGCTGGGATCTTTGCTATAATC 961  
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Db 833 TTTGCTGCACTATCCATGATGATGAGCAGCAGGCGCACTACCAACAGCTTCCACATCCAG 892

Db 962 TTCTCAGCTGCCATCCACTACTAGAGCATACCGGAACCAACAAATTTCCACATTCAG 1021  
 QY 893 ACCAAGTCAGATGCGCATCGTGTACAAATGATCTTCAGTCTCGGAATCACCACATC 952  
 Db 1022 ACTCGGTGATCCAGCTATTCTGTATATACAGATCTGACTGGGAATCACCATTTA 1081  
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 Db 1082 AGTGCAGCTTATCGCTTCTGCAAGATGACGAGGAATGAATATTTGATTAACCTTCA 1141  
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 Db 1142 AAGGATGAGTTGTAGAACTCGAGCCCTGCTGATGAGATGAGATGAGATGAGATGAG 1201  
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 Db 1202 TCTGTCACTTCCACAAATCAAGCAATGAAGACTGCTGACAGCAGATATTTAGCCATCCAGCAAAA 1261  
 QY 1130 GACAAGCCAAAGGCGCTGCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189  
 Db 1262 GAAAAGCCAAAGCGCTTATCCCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321  
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 Db 1322 GATGGGACCTCCATCATCGCTGGGAATGCTCACTCTCGGAGGATTTCTTCAGACAGGT 1381  
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 Db 1382 GACAGAGAGCAGAGCTGGGCTGCTTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1441  
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 QY 1370 ACTGAGCTGGCAGAGAGTGTTCAGCCCTGCGGATGAGGACTTCAAGTCT 1423  
 Db 1502 ACGGACATGACCGAGAGATTGTGAGTCCATTAATCGATGAACCTCTCAACT 1555

RESULT 15

US-08-455-525-50

; Sequence 50, Application US/08455525

; Patent No. 5800987

; GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.

; APPLICANT: Bentley, Kelley

; APPLICANT: Charbonneau, Harry

; APPLICANT: Sonnenburg, William K.

; TITLE OF INVENTION: DNA Encoding Mammalian

; TITLE OF INVENTION: Phosphodiesterases

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; STREET: Street

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,525

; FILING DATE: 31-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/297,494

; FILING DATE:

; APPLICATION NUMBER: US 07/688,356

; FILING DATE: 04-APR-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 5800987and, Greta E.  
 ; REGISTRATION NUMBER: 35,302  
 ; REFERENCE/DOCKET NUMBER: 27866/30822  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (312) 346-5750  
 ; TELEFAX: (312) 984-9740  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 50:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2693 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 176..2077  
 ; US-08-455-525-50

Query Match 19.3%; Score 598; DB 1; Length 2693;  
 Best Local Similarity 67.9%; Pred. No. 2.4e-154;  
 Matches 851; Conservative 0; Mismatches 400; Indels 3; Gaps 1;

QY 173 AGGCTGCGCTACATGCTGAAGCAGTTGGAGAAATGGGAGATAAAACATTTGAGGAGCTGAAG 232  
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Job time : 206 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY\_NUC  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	579.8	18.8	2656	10	US-09-883-825-16
5	578.8	18.7	1625	10	US-09-883-825-48
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7	449.6	14.5	2077	10	US-09-883-825-52
8	348	11.3	412	10	US-09-883-825-22
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					Sequence 2175, Ap
					Sequence 1023, Ap
					Sequence 22257, A
					Sequence 11178, A
					Sequence 6, Appl
					Sequence 22, Appl

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35	68.8	2.2	4131	10	US-09-883-825-38	Sequence 38, Appl
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37	66.4	2.1	915	11	US-09-989-442-48	Sequence 48, Appl
38	63	2.0	3221	9	US-09-815-825-19	Sequence 19, Appl
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## ALIGNMENTS

## RESULT 1

US-09-883-825-26  
; Sequence 26, Application US/09883825  
; Patent No. US20020151024A1  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; Bentley, Kelley  
; Charbonneau, Harry  
; Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/883,825  
; FILING DATE: 18-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/123,783  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/297,494  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20020151024A1and, Greta E.

REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1844 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:

NAME/KEY: CDS  
LOCATION: 114..1715

SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-883-825-26

Query Match 43.6%; Score 1347.6; DB 10; Length 1844;  
Best Local Similarity 90.6%; Pred. No. 0;  
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

175 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 234  
176 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 283  
177 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 294  
178 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 343  
179 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 354  
180 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 403  
181 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 414  
182 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 460  
183 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 474  
184 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 520  
185 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 534  
186 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 580  
187 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 594  
188 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 640  
189 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 654  
190 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 700  
191 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 714  
192 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 760  
193 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 774  
194 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 820  
195 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 834  
196 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 880  
197 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 894  
198 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 940  
199 GCTGGCTACATGGTGAAGCAGTTGGAGATGGGAGATGAACATTTGAGGAGCTGAAGAA 954

941 (AAATCGGAATGCGCATCTCTGTACAAAGACCGCTCAGTGCTGCTGAGAAATCACCACATCAG 1000  
942 (CTGTGTTTTCGATTGATGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014  
943 (CTCGTTTTCGAAATGATGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1060  
944 (TGAGTTTGTAGAACTCCGAGCCCTGGTTCATGATGATGATGATGATGATGATGATGATGATGAT 1074  
945 (TGAGTTTGTAGAGCTGCGGCTCTGGTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1120  
946 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1134  
947 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1180  
948 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1194  
949 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1240  
950 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1254  
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952 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1314  
953 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1360  
954 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1374  
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956 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1434  
957 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1480  
958 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1494  
959 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1540  
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961 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1600  
962 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1614  
963 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1660  
964 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1674  
965 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1719  
966 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1734  
967 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1777  
968 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1791  
969 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1799  
970 (CATTTCCAGCAAGTGAAGCATTGAAGACAGCTTGCAGCAGCTGAGAGATGATGATGATGATGAT 1837

## RESULT 2

US-10-027-632-21270/C  
Sequence 21270, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
POLYMORPHISMS IN THE HUMAN GENOME  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30





us-09-663-481-2.rnpb

Mon Aug 11 15:23:54 2003

1502 ACGGACATGACCGAGAGATTTGTGAGTCCATTAATCGATGAACCTCTCAAACT 1555

Db	422	CTCCTGGATACAGAGATGAGCTCAGTACATTCAGTCAGATGCTGTGCTTCTGAGTC 481
Qy	353	CGGACTGCTGGCTCCACCTTCCAGCAGGCGCGGCGCAAGGCGCGCGAGCAG 412
Db	482	CGAGACTGCTGGCTCCACCTTCCAGCAGGCGCGGAGATGGGATGATGCTCAGGAGGCGC 541
Qy	413	GAGAAGCCCAAGTTCGGAAGCATTTGTCAGCTGTGCGAGCTGGGATCTTGTGGAAGG 472
Db	542	GAGAAGCCCGGTTCAAGAGCATCGTTACGAGCTGCGAGCTGGGATATTTGGGAGA 601
Qy	473	ATGTTCCGGAGAACATACACCTCTGTGGGCCCCACTTACTACTGCGGTTCTCACTGT 532
Db	602	ATGTATAGACGGACATCAACATGTTGGAGTGAGCTATCCACGACTTTATTTAGGCA 661
Qy	533	CTCAAGAACCTGGATCTCTGGTCTTGTGATGCTTTTCTTGTGACCGAGCAGATGAC 592
Db	662	TTAAAGGATGTGACAGTGTCTTTGAGTCTTGTGAGCTTTTCCCTCAATGAGGCCAGTGGAT 721
Qy	593	CATGCTCGAGGACATTTGTTGATGCTGCTGACTCGGATTAACCTATCAGCGCTTC 652
Db	722	CATGCACTGAAATTTATTTCTATGAATCTACTCAGCTTTGATCTGATCAGCGCTTC 781
Qy	653	AAGATCCCACTGTTTGTGATGAGTTCCTGATGCTTGTGAGCTGAGCAGCTATGGAAG 712
Db	782	AAGATCCCACTTCTGCACTGCTCTCAITTTGGAGGCCCTGGAAGTGGATACAGCAAG 841
Qy	713	TACAGAACTCTTACCAACAGATCAGCAGCGCATGTATTACCAAGCAGTCCATTGC 772
Db	842	CACAAAATCTTACCAATATTTATGCACTGCTGCGCATTTTACACAGACAGTGCATTAC 901
Qy	773	TTCTTGTCCGCGAGGATGTTGCTGCTGCTGCGAGATTTGAGTGTGCTGCGCATCATC 832
Db	902	CTCTCTTATAGCAGGAGTGGCACTTGGCTGAGGAGCTGGAGATTTTGTCTATATC 961
Qy	833	TTTGTGAGCTATCCATGATATGACGACAGCGGCACTTACCAAGCAGTTCACATCCAG 892
Db	962	TTCTGAGCTGCACTCATGATACGAGCATACCGGAACCAACCAAAATTTCCACATTCAG 1021
Qy	893	ACCAAGTCAAGTGTGCCATCTGTACATGATCTGCTGAGTGTGCTGCGGAAATCACACATC 952
Db	1022	ATCTGCTGATCCAGCTATTCTGTATATGATGATGATGATGATGATGATGATGATGAT 1081
Qy	953	AGCTCTGTTTCCGATTGATGAGGATGATGAG---ATGAACATTTTTCATCAACCTACC 1009
Db	1082	ATGTCAGCTTATCGCTTCTGCAAGATGACGAGGAATGAATATTTGATTAACCTCTCA 1141
Qy	1010	AAGATGAGTTTCTAGAACTCCGAGCCCTGGTCAATGATGATGATGATGATGATGATGAT 1069
Db	1142	AAGATGAGTGGAGGAGTTTCGAACCTTGGTAATGAAATGAAATGAAATGAAATGAAATG 1201
Qy	1070	TCCTGCTATTTCCAGCAAGTGAAGACCATGAAGACAGCCCTTGAACAGCTGGAGGAT 1129
Db	1202	TCCTGCTATTTCCAAACAAATCAAGCAATGAAGACTGCTCTGAGCAGCGCAGGCAAT 1261
Qy	1130	GACAAGCCCAAGCCCTCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1189
Db	1262	GAAGAAGCAAAAGCTTATCCCTATGCTGATGATGATGATGATGATGATGATGATGATG 1321
Qy	1190	CAGTGGTGTGTCACAGCCGTTGACCAAGCCCTCATGAGAGANTCTTCCCTCAGGT 1249
Db	1322	GCATGGGACCTTCCATATCGCTGAGCAATGCTCTGAGGAGGATTTTTCAGACAGGT 1381
Qy	1250	GACAAGGAGGAGAGTGGGCTGCTCTTCTCCATCTCTGCTGCTGCTGCTGCTGCTGCTG 1309
Db	1382	GACAGAGAGCAGAGCTGGGCTGCTTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1441
Qy	1310	GTGGCAGATCTCAGATAGGTTTATCGACTGATGTTGGAGCCCATTTCTGTGTGTG 1369
Db	1442	GTGTGCTAGTCAAGATAGGTTTCAATGTTTATCTGCTGAGCAACCTTTCACGTGCT 1501
Qy	1370	ACTGAGCTGGCAGAGAGTGTTCAGCCCTTGGCGGATGAGGACTCCAACT 1423

RESULT 4

US-09-883-825-16

Sequence 16, Application US/09883825

Patent No. US20020151024A1

GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.

Bentley, Kelley

Charbonneau, Harry

Sonnenburg, William K.

Mammalian

TITLE OF INVENTION: DNA encoding Phosphodiesterases

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Coole, Gerstein, Murray &

STREET: Two First National Plaza, 20 South Clark

Street

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60609

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/883,825

FILING DATE: 18-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION NUMBER: 09/123,783

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/297,494

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/688,356

FILING DATE: 04-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: No. US20020151024Aland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30822

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 2656 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLFCULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 136..1677

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-883-825-16

Query Match 18.8%; Score 579.8; DB 10; Length 2656;

Best Local Similarity 64.8%; Pred No. 1.3e-165;

Matches 883; Conservative 0; Mismatches 472; Indels 0; Gaps 0;

Qy 101 AAGCAGAACTTTGATTCCTCCATGGCAACCTGTTCTCTGTCAGAGGAGCCACCTCCAG 160

Db 115 AAGCTAACTTTCCACCTTTAAATGGATGACCATGTCCAAATCAGGAGGAAACATCTCCAA 174

Qy 161 GGCCCATTTCTAGCTGCGCTACATGGTGAACACCTTGGAGATGGGAGATAAACATT 220

Db 175 AGACCATCTTAGACTAAGATGCTTAGTGAAGCAGCTGGAAGAAAGGTGATGTTAACGTC 234

QY 221 GAGGAGCTGAAGAAAAAATCTGGAGTACACAGCTCTCTCTGCTGGAAGCCGCTACATAGAT 280  
DB 235 ATCGACTTAAAGAAATATTAATATGACGACTCTGTGTTGGAAGCAGTTTATATGAT 294  
QY 281 GAGACAGCGCAATCTTGGACACGAGGACAGCTGCGGCTGAGATCGCGTG 340  
DB 295 GAACAGAGGAGCTGCTGGACACGAGTATGAGCTGAGTACATGCTGCGATTCGCTG 354  
QY 341 CTTTCGGAGTGGCGGAGCTGCTGCTGCTCCACCTTCCACCCAGCAGCGCCGCGCAAGGC 400  
DB 355 CCATCAGAAGTCCGGAGCTGTTGGCTTCTACCTTTACACGGAATGGGATGATGAA 414  
QY 401 CGCCGACAGAGGAGAGCCCAAGTTCGGAAGCATTTGTCACGCTGTGACGCTGGGATC 460  
DB 415 AAGAAATCTGAGGAAAAACCAAGATTTCCGAGCATTTGTCATGTTGTTCAAGCTGGAAT 474  
QY 461 TTCGTGGAACGATGTTCCGAGAACATACACCTCTCTGGGCCCCCACTTACTCTACGCG 520  
DB 475 TTTGTGGAAGATGTACAGAAAGTCTTATCACAATGTTGGCTTGGCATATCCAGAGGCT 534  
QY 521 GTTCTCAACTCTCAAGAACTGATCTCTGCTGCTTTGATGCTTTTCTTTCCTTGAACCCAG 580  
DB 535 GTCATGTAACATTAAGAGTGTGATAAATGGTCTTTGATGATGATTTGCTTGAATGAA 594  
QY 581 GCAGAGATGACCATGCGCTGAGGACCATGTTTGTGATGCTGCTGCTGCTGCTGCTGCT 640  
DB 595 GCAAGTGGAGAACACAGCTGCTGAAGTTTATGATTTATGAATCTTACCCAGATATGATCT 654  
QY 641 ATCAGCCGCTTCAAGATTTCCACCTGCTGTTTGTGATGATGCTTCTGCTGCTGCTGCTG 700  
DB 655 ATCAACCGCTTCAAGATTTCTGCTTCTGCTTATGCTTGTGCTTGTGCTGCTGCTGCTGCT 714  
QY 701 GGCTATGGGAAGTACAAGAACTTACCACAAACAGATCCACGACCGGATGTTTACCACAG 760  
DB 715 GGTACAGCAAGTACAAAATCCATACCAATTTGATTCATGACGCTGATGCTACITCAA 774  
QY 761 ACAGTCAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820  
DB 775 ACTGCTATACATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 834  
QY 821 CTGCGCATCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 880  
DB 835 TTGACATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894  
QY 881 TTCCACATCCAGCAAGTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 940  
DB 895 TTTACATTCAGACAAAGTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 954  
QY 941 AATCACCACATCAGCTCTGTTTCCGATGATGAGGATGATGATGATGATGATGATGATGAT 1000  
DB 955 AATCATCATGTGAGTGCAGCTTATCGCTTATGCAAGAAAGAAATGAATGCTCTGATA 1014  
QY 1001 AACCTCACAAGGATGATGTTGTAGAACTCCGACCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1060  
DB 1015 AATTATTCGAAGATGATGAGGAGCTTCCGAACTGATGATGATGATGATGATGATGATGATG 1074  
QY 1061 ACAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120  
DB 1075 ACAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1134  
QY 1121 GAGAGGATGACAAAGCCCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1180  
DB 1135 GAAGGGCTTGACAAAGCCCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194  
QY 1181 CCAACCAAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240  
DB 1195 CCAGCCAAATCTGGAAGCTGACACCGATGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254  
QY 1241 CGTCAGGATGACAAAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1300  
DB 1255 CTACAGGAGATGAAGAGCTGAATAGGGCTTCCATTTCCCGCTGCTGCTGCTGCTGCTGCTG 1314  
QY 1301 TCCACTGTAGGCGACAGTCTCAGATAGAGGGTTCATGCTGCTGCTGCTGCTGCTGCTGCTG 1360

DB 1315 TCAACGATGTTGGCCAGTCCCAATAGTTTCATTTTCATAGTAGAACAACATTT 1374  
QY 1361 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420  
DB 1375 TCTCTCTGACAGACTCAACAGAGAAATTTATTTCTCTTATAGAGAAAGACTCGAAA 1434  
QY 1421 TCTAAAAACCCAGCCC 1435  
DB 1435 ACCAAAACCTCTCC 1449

## RESULT 5

US-09-883-825-48  
; Sequence 48, Application US/09883825  
; Patent No. US20020151024A1  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; Bentley, Kelley  
; Charbonneau, Harry  
; Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/883,825  
; FILING DATE: 18-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/123,783  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/297,494  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20020151024A1and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1625 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 12..1616  
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:  
US-09-883-825-48

Query Match 18.7%; Score 578.8; DB 10; Length 1625;  
Best Local Similarity 66.0%; Pred. NO. 2e-165;  
Matches 838; Conservative 0; Mismatches 432; Indels 0; Gaps 0;





us-09-663-481-2.rnpb

Mon Aug 11 15:23:54 2003

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; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..1693
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-883-825-52
    Query Match      14.5%; Score 449.6; DB 10; Length 2077;
    Best Local Similarity 68.0%; Pred. No. 5.6e-126;
    Matches 642; Conservative 0; Mismatches 299; Indels 3; Gaps 1;

483 GAACATACACCTCTGTGGGCCCCACCTACTACTACTGCGGTCTCTCACTGTCACGAACC 542
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
543 TGGATCTCTGGTCTTGTATGCTTTCTTCTTGAACGAGCAGACATGACCATGCCCTGA 602
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
63 TGGACAGTGTGCTTGTGAGCTTCTTCTCTCTCATGAGCCAGTGGGGATCAGCTGA 122
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
603 GGACCAATGTTTGTGAGTGTGAGCTGCGCATCACTCATCGCCGCTTCAAGATTCCCA 662
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
123 ATTTATTTCTATGACTACTCACAGCTTATGATCTGATCAGCCGCTTCAAGATCCCA 182
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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663 CTGTGTTTGTATGAGTTCTTCTGATGCTTGGAGACAGCTATGGAAGTACAAGAATC 722
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
183 TTCTGCACTTGTCTCATTTGTGGAGCCCTGGAAGTGGATACAGCAAGCACAAAATC 242
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
723 CTTACACACAGCAGTCCAGCAGCGATGTTTACCCAGACAGTCCATTGCTTCTGCTCC 782
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
243 CTTACCATACTTAATGCAGCTGCCGATCTTACACAGACAGTGCATTACCTCTCTATA 302
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
783 GCACAGGAGTGTGCTGCTGCTGCGGAGATGAGCTCCTGGCCATCATCTTTGCTGCAG 842
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
303 AGACAGGAGTGGCAACTGGCTGACGGAGCTGGAGATCTTTGCTATTAATCTTCTCAGCTG 362
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
843 CTATCCATGATTATGACACAGCGGCACATCCACACAGCTTCCACATCCAGACCAAGTCAG 902
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
363 CCATCATGACTACGAGCATACCGGAACACCAACAATTTCCACATTCAGACTCGGTCTG 422
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
903 AATGTGCCATCGTGTACATGATCGTTCAGTGTCTGGAGAAATCACACATCAGCTCTCTTT 962
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
423 ATCCAGCTATTCTGTATAACACAGATCTGTACTGGAGAAATCAACATTAAGTGCAGCTT 482
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
963 TCCGATTCATGACGAGATGATGAG--ATGAAATTTTTCATCAACTCCACCAAGATGAGT 1019
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
483 ATCGCCTTCTGCAAGATCAGGAGAAATGAATTTTGAATTAACCTCTCAAGATGACT 542
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1020 TTGTAGAACTCGAGCCCTGGTCAATGATGATGTTGGCCACAGATGCTCTGCCATTT 1079
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
543 GGAGGGAGTTTCCAACTTGGTAATGAAATGGTGTGGCCACAGATATGCTTGTCACT 602
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1080 TCCAGCAAGTGAAGACCATGAGACAGCCTTGCAACAGCTGAGAGGATTCACAGGCCA 1139
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
603 TCCAAACAATCAAGCAATGAAGACTGCTGACAGCAGCAGAGCCATGAAGCCAA 662
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1140 AGGCCCTGTCTACTGTCTCCATGCTGTGATCAGATCAGCCACCAAGCAGTGGTGG 1199
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
663 AAGCCTTATCCCTTATGCTGATACAGAGATATTAGCCATCCAGAAAGCATGGGACC 722
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1200 TCCACAGCGGTGGACCAAGGCCCTCATGAGAGAAATTCCTCGTCAGGTGACAGGAGG 1259
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
723 TCCATCATCGCTGGCAATGTCTCTCTGGAGAGTCTTCACAGAGGTGACAGAGAG 782
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1260 CAGAGTGGGCTGCGCCTTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGGCAGAT 1319
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
783 CAGAGCTGGGGTGGCCTTTTCTCTCTGTGTGACGAAAGTCCACTATGTGTCTCAGT 842
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1320 CTCAGATAGGTTTCACTGCACTTCAITGTGGAGCCCACTTCTGTGTGCTGACTGAGTGG 1379
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
843 CACAAGTAGGTTTCAITGTATGATCATGCTGGAACCCACCTTCACTGTGCTTACGAGATGA 902
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1380 CAGAGAGAGTGTTCAGCCCTTGGCGGATGAGAGCTTCCAGTCT 1423
QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Mon Aug 11 15:23:54 2003

Db 1259 CACCAAGAGAGCGCTGACAGACTCAGGAAGATGGTTATGACATGGTTAGCAACGTA 1318  
Qy 1066 CATGCTCCGATTTCCAGCAAGTGAAGACCAATGAAGA----- 1103  
Db 1319 TATGCTAAACATATGAGCGCTCTGCGAGACCTGAGACAATGGTTAGAAAGAAAGT 1378  
Qy 1104 -----CAGCCTTGCAACAGCTGGAGAGGATTCAGAGCCCA---AGGCCCTGCTCT 1152  
Db 1379 TACAAAGTTCAGCGGTTCTTCTCTAGACACACTATACCGATCGCATTCAGCTTCGCA 1438  
Qy 1153 ACTGCTCCATGCTGCGACATGAGCGACCCACACAGAGTGGTCCACAGCGGTG 1212  
Db 1439 CATGGTACACTGTCAGACACTGAGCAACCCACCAAGTCTCTTGAATTCATCGCAATG 1498  
Qy 1213 GACCAAGGCCCTCATGAGGAATTCCTCGTCAGGTGACAAAGGAGGAGAGTTGGGCT 1272  
Db 1499 GACAGCCGATCATGAGGAATTTTCCAGCAGGAGGAGACAAAGCGGGAGAGGGAAT 1558  
Qy 1273 GCCCTTTCCTCACTCTGTGACCGCACTTCCACTCTAGTGGCACAGCTCAGATAGGTT 1332  
Db 1559 GGAATTAGCCCAATGTGTATAACACACAGCTTCTGTGGAATAATCCAGGTTGGTT 1618  
Qy 1333 CATCGACTTCATGTGAGCCCACTTCTCTGTGCTGACTGACGTGGCAGAGAGAGTGT 1392  
Db 1619 CATCGACTACATGTCATCCATTTGTTGGAGACATGGCGAGATTTGGTACAGCCTGATG 1678  
Qy 1393 TCAGCCCTGGCGGAT 1408  
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RESULT 11

US-09-880-107-2175  
; Sequence 2175, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 4921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2175  
; LENGTH: 3705  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L20965  
US-09-880-107-2175

Query Match 5.3%; Score 165.2; DB 10; Length 3705;  
Best Local Similarity 52.1%; Pred. No. 3.6e-39;  
Matches 445; Conservative 0; Mismatches 373; Indels 36; Gaps 2;  
  
Qy 533 CTCAGAAGCTGGATCTGTGGCTTTGATGCTTTCTTCTTGAACGCGCAGATGAC 592  
Db 1220 CTGAGAAGCTGAACAGTGGGCGCGGAACATCTTTGGCTGTGCGATACCTGGAGC 1279  
Qy 593 CATGCCCTGAGGACCAATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652  
Db 1280 CGTCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1339  
Qy 653 AAGATCCCACTGTTTGTGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712

Db 1340 CGCATCCGCTGGACACGATGGTGACATACATGCTGACGCTGGAGGATCACTACCAAGCT 1399  
Qy 713 ACAAGAACTCTTACCACAAACAGATCCAGCGAGCCGATGTTACCCAGAGATCCATTCG 772  
Db 1400 GACGTG---GCCTACCAATAACAGCGCTGACGAGCTGCTGCTGCTGCTGCTGCTGCTG 1456  
Qy 773 TCTTGTCTCCGACAGGATGGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 832  
Db 1457 TGTCTGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1516  
Qy 833 TTTGCTGAGTATCCATGATATGAGCACAAGGCGCTACCAACAGCTTCCACATCCAG 892  
Db 1517 TCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1576  
Qy 893 ACCAAGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952  
Db 1577 ACCAATTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1636  
Qy 953 AGCTCTGTTTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1012  
Db 1637 GCGGTGGCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1696  
Qy 1013 GATGATTTGTAGAACTCCGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1072  
Db 1697 CCGCAGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1756  
Qy 1073 TCGCATTTCCAGAGTGAAGACCATGAAGACAGCTTGAAGACAGCTGCTGCTGCTGCTG 1129  
Db 1757 AAGCATGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1816  
Qy 1130 -----GACAAGCCCCAAGGCCCTGCTCTACTGCTC 1159  
Db 1817 TCAGGGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1876  
Qy 1160 CATGCTGCTGACATCAGCCACCAACAGCAGTGGTTCACACAGCGCTTGGACCAAG 1219  
Db 1877 CACTGTGCCGACCTCAGCAACCCACCAAGCCCTGGAGCTGTGTACCGCCAGTGGACAGAC 1936  
Qy 1220 GCGCTCATGAGGAATTTCTTCCGTGAGGTGACAAGGAGGAGGAGTGGGCGCTGCGCTTT 1279  
Db 1937 CGCATCATGCGCGAGTTCTTCCAGAGGCTGACCGAGCGCGCGCTGGCATGGAAATC 1996  
Qy 1280 TCTCCACTCTGTACCGCACTTCCACTCTAGTGGCAGCTCTCAGATAGGTTTCATCGAC 1339  
Db 1997 AGCCCATGTGTGACAAGCACACTGCTCGTGGAGAAAGTCTCAGGTGGGTTTTATTGAC 2056  
Qy 1340 TTCATTTGGAGCC 1353  
Db 2057 TACATTTGCACCC 2070

RESULT 12

US-09-954-531-1023  
; Sequence 1023, Application US/09954531  
; Patent No. US20020165180A1  
; GENERAL INFORMATION:  
; APPLICANT: Weaver, Zoe  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using  
; TITLE OF INVENTION: Gene Sets  
; FILE REFERENCE: 689290-77  
; CURRENT APPLICATION NUMBER: US/09/954,531  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: US/60/233,133  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,009  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,034  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,509  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US/60/234,567  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 1392



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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1023
; LENGTH: 3705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-1023

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Query Match 5.3%; Score 165.2; DB 10; Length 3705;  
Best Local Similarity 52.1%; Pred. No. 3.6e-39;  
Matches 445; Conservative 0; Mismatches 373; Indels 36; Gaps 2;

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US-09-918-995-22257
; Sequence 22257, Application US/09918995
; Publication No. US20030073623A1
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; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22257
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(445)
; OTHER INFORMATION: n = A,T,C or G
;
US-09-918-995-22257

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Mon Aug 11 15:23:54 2003

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; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11178
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006377.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.53
US-09-664-761-11178

Query Match
Best Local Similarity 3.3%; Score 101.8; DB 9; Length 470;
Matches 133; Conservative 71.9%; Pred. No. 2.7e-20;
Mismatches 52; Indels 0; Gaps 0;

QY 288 GCAATCTTGACACGAGGACGAGCTGCAGGAGCTCGGTTCAGATCCGCTGCTCGG 347
Db 433 GGAGACTCTGTATACAGAGGATGAGCTCAGTGCATTCAGTACAGATCTGTGCTCTG 374

QY 348 AGTGGGAGCTGGCTGGCTCCACCTTCCAGGAGCTGTCAGCTGTGAGGAGGAGGAG 407
Db 373 AGTGGGAGCTGGCTGGCTCCACCTTCCAGGAGCTGTCAGCTGTGAGGAGGAGGAG 314

QY 408 CAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 467
Db 313 GCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 254

QY 468 AACGG 472
Db 253 AGAGG 249

RESULT 15
US-09-666-781A-6
; Sequence 6, Application US/09966781A
; Publication No. US20030036184A1
; GENERAL INFORMATION:
; APPLICANT: SOULARD, PATRICIA
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
; TITLE OF INVENTION: SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY
; FILE REFERENCE: A000028105
; CURRENT APPLICATION NUMBER: US/09/966,781A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP004026837

; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1231
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-966-781A-6

Query Match
Best Local Similarity 3.2%; Score 98.2; DB 11; Length 1281;
Matches 415; Conservative 47.9%; Pred. No. 5.6e-19;
Mismatches 438; Indels 14; Gaps 4;

QY 533 CTCAGAACCTGGATCTCTGGTGGCTTTCAGTTCGCTCGGATACCTTCAACGAGGAGGAGATGAC 592
Db 274 CTGGAAAGATGGAAATGGAAATGGAAATGGAAATGGAAATGGAAATGGAAATGGAAATGGAAAT 333

QY 593 CATGCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 652
Db 334 AATAGTCTAGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 393

QY 653 AAGATCCCACTGTGTTTTCAGTTCGCTCGGATACCTTCAACGAGGAGGAGGAGGAGGAGGAGGAG 712
Db 394 CATTTAGATATGGTGAACCTCCGTCGATTTTAGTT---ATGATTCAAGAGAGATTACCCAC 450

QY 713 TACAGAGATCTTACCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 772
Db 451 AGTCAAAATCTTACCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 510

QY 773 TTCTTGGCTCCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 832
Db 511 TACTTAAGGAACCTAAGCTTGGCAATTTCTGAATCTTGGGATATCTTGTGAGCTTA 570

QY 833 TTTGCTGAGCTATCCATGATATGAGCACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 892
Db 571 ATTGAGCTGCCACTCATGATCTGGATCACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 630

QY 893 ACCAAGTCAGAAATGTCATCTGTCACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 952
Db 631 ACCAACCATTACTTGGCAACTTATACAGAAATACCTCAGTCTCGGAGGAGGAGGAGGAGGAGGAGGAG 690

QY 953 AGCTCTCTTTTCCGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1006
Db 691 AGATCTCCGCTGGCTTGTGAGAGAACTGGTCTGTCTCAGACATCTGCCATTTGGAAGC 750

QY 1007 ACCAAGATGAGTTTGTAGAACTCCGAGCCCTGGTCAATTGAGATGG---TGTTGGCCAC 1062
Db 751 AGGCATGAGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 810

QY 1063 AGACATGTCCTGTCATTTCCAGCAAGTGAAGACCATGAAGACACCTTGCAGAGCTGGA 1122
Db 811 AATGAGTACCTGTCTATTTTGTAGATCTCACTTGGATGAAG---GTGACTTACCTTACCTGAGCA 869

QY 1123 GAGGATTCAGAACCCCAAGCCCTGTCTTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
Db 870 TGGCAGACATAGGCAATTTGGTTTACAGATGGCCCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 929

QY 1183 AACCAAGCAGTGGTTGGTCCACAGCCGTTGGCCCTGACCAAGCCCTGACGAGGAGGAGGAGGAGGAGGAG 1242
Db 930 ATGTCCGAACCTGGGAATTAAGCAAGCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 989

QY 1243 TCAGGATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1302
Db 990 CCAAGGCGATATAGAAAAAGTACCATTTGGTGTGAGTCCATTTGGTGTGAGTCCATTTGTTGATCC 1049

QY 1303 CACTCTAGTGGCAGAGTCTCAGATAGGTTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGAT 1362
Db 1050 TGAGTCTATTTGCAACATCCAGATTTGGTTTATGACTTACCTTACCTTACCTTACCTTACCTTACCTT 1109

QY 1363 TGTGCTGACTGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1389
Db 1110 AGAGTGGCCAGGTTTTCACACAGG 1136
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Mon Aug 11 15:23:54 2003

us-09-663-481-2.rnpb

Page 13

Search completed: August 11, 2003, 01:06:30  
Job time : 683 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 17:33:05 ; Search time 5699 Seconds

(without alignments)  
13182.161 Million cell updates/sec

Title: US-09-663-481-2

Perfect score: 3091

Sequence: 1 gtcgccaccagctccggga.....aaaaaaaaaaaaaaaaaaaaa 3091

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*\*

2: em\_esthum:\*\*

3: em\_estin:\*\*

4: em\_estmu:\*\*

5: em\_estov:\*\*

6: em\_estpl:\*\*

7: em\_estro:\*\*

8: em\_estc:\*\*

9: gb\_est1:\*\*

10: gb\_est2:\*\*

11: gb\_estc:\*\*

12: gb\_est3:\*\*

13: gb\_est4:\*\*

14: gb\_est5:\*\*

15: em\_estfun:\*\*

16: em\_estom:\*\*

17: em\_gss\_hum:\*\*

18: em\_gss\_inv:\*\*

19: em\_gss\_pln:\*\*

20: em\_gss\_vrt:\*\*

21: em\_gss\_fun:\*\*

22: em\_gss\_mam:\*\*

23: em\_gss\_mus:\*\*

24: em\_gss\_pro:\*\*

25: em\_gss\_rod:\*\*

26: em\_gss\_phg:\*\*

27: em\_gss\_vrl:\*\*

28: gb\_gss1:\*\*

29: gb\_gss2:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	734	23.7	786	12 B1488476	B1488476 603020977
3	665.2	21.5	878	10 BG390932	BG390932 602417604
4	643.4	20.8	749	13 BQ179638	BQ179638 UI-M-EVO-

5	636.8	20.6	737	13	BQ179626	BQ179626 UI-M-EVO-
6	600	19.4	2053	11	AK014887	AK014887 Mus muscu
7	600	19.4	2132	11	AK077123	AK077123 Mus muscu
8	599.6	19.4	2128	11	AK015375	AK015375 Mus muscu
9	599.6	19.4	3451	11	AK050499	AK050499 Mus muscu
10	599.6	19.4	3909	11	AK030423	AK030423 Mus muscu
11	599.6	19.4	4017	11	AK082180	AK082180 Mus muscu
12	599.6	19.4	4484	11	AK082497	AK082497 Mus muscu
13	599.6	19.4	4729	11	AK029531	AK029531 Mus muscu
14	593	19.2	4273	11	AK043647	AK043647 Mus muscu
15	588.8	19.0	650	10	BG698525	BG698525 602658855
16	586.6	19.0	593	14	CA308319	CA308319 UI-H-FTL-
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18	550.4	17.8	554	14	CA397265	CA397265 cs89a07.y
19	543.2	17.6	688	13	BQ573665	BQ573665 UI-M-FD0-
20	538	17.4	538	14	CB155259	CB155259 K-EST0213
21	516.6	16.7	571	10	AW961995	AW961995 EST374068
22	506.4	16.4	515	12	BM875524	BM875524 Ij34a09.y
23	501.8	16.2	1607	11	AK014810	AK014810 Mus muscu
24	497	16.1	497	14	CA395159	CA395159 cs61a04.y
25	482	15.6	566	14	BY704970	BY704970 BY704970
26	479	15.5	571	14	CB615459	CB615459 AMGNNUC:N
27	473.6	15.3	712	12	B1738670	B1738670 603358893
28	469.4	15.2	821	12	B1758291	B1758291 603029943
29	461.6	14.9	743	14	CD354171	CD354171 UI-M-GM0-
30	461	14.9	461	13	BX113721	BX113721 BX113721
31	455.8	14.7	1153	12	BM544206	BM544206 AGENCOURT
32	444.4	14.4	456	12	BM875274	BM875274 Ij54a09.x
33	421.8	13.6	573	10	BF045437	BF045437 BP250016B
34	414	13.4	414	14	CA392998	CA392998 CS32B09.y
35	412.6	13.3	603	13	BQ830217	BQ830217 LL61n1072
36	381.6	12.3	474	14	R35320	R35320 Y965a07.r1
37	375	12.1	439	14	R48984	R48984 Y965a07.s1
38	373.6	12.1	807	14	CA316824	CA316824 UI-M-FM0-
39	372.4	12.0	448	14	H51115	H51115 Y032C02.s1
40	371.8	12.0	783	13	BQ571565	BQ571565 UI-M-FC0-
41	368.6	11.9	459	9	AW489593	AW489593 UI-M-BH3-
42	359.6	11.6	458	13	BQ829442	BQ829442 LL61n2036
43	357.4	11.6	874	13	BQ894022	BQ894022 AGENCOURT
44	357	11.5	562	10	BE756527	BE756527 210694 MA
45	354.6	11.5	554	10	BF076938	BF076938 226709 MA

#### ALIGNMENTS

RESULT 1  
AK004772  
LOCUS  
DEFINITION  
AK004772 2808 bp mRNA linear HTC 05-DEC-2002  
Mus musculus adult male lung cDNA, RIKEN full-length enriched  
library, clone:1200014008 product:phosphodiesterase 1B,  
Ca2+-calmodulin dependent, 63 kDa, full insert sequence.

ACCESSION  
AK004772.1 GI:12836202

VERSION  
AK004772.1 GI:12836202

KEYWORDS  
HTC; CAP trapper.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)

2  
99279253  
10349636

REFERENCE  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL  
Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE  
20499374

PUBMED  
11042159





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Db      2479  TTCCCC-----TCCGGGGCCCTCGTGGTGGAGGAGATGGGGAGGGCTCAGGCG 2533
Qy      2747  CTGCTGCTTCCTGTCCTGAGAGAACCCAGCCAGGCGGCTGCCCTTCTCTCCCTC 2806
Db      2534  GGTAGCAACTGGAGACACCAGAGCGAGTGCAGCCAGGTAAA--GCCTCTCTCTGTCCTC 2591
Qy      2807  AGGCTCTCTCTGCCCCCAGCTTGGCCCCAGGAAAGCCCAAGTCCAGGTGACTGCCCTCC 2866
Db      2592  AGGCTCC-----TTGGCCCCAGCTCACCCCATTTAAGGCC--AGTCCAGGTGACTG-CCTCC 2645
Qy      2867  TTCTTTCTTTAAATACCAACCATGATGATTTGTACAGTGGGCCCTGTGTATGGAATCCA 2926
Db      2646  TCTCTCTCTTTAAATA-----CATGATTTGTACAGTGGGCCCTGTCTTTGTAAGTCCA 2700
Qy      2927  CATCCATGTCCTCTAGACCTGTACCCCTGGTACTTCCACCCCTACCCACCCCGAGAAGG 2986
Db      2701  TCTCCATGGTTC-ATTAGACCTGCCACTCT----- 2728
Qy      2987  GCAGAGACGATGTGACTACCCCTGCTGCTTTCCAGACCCCTGCTATAGCCAGAG 3046
Db      2729  ---GAACCGCATGTGACTCCCTCCCATGCTCTTGTGCTCTCCAGGCCCTGCTATAGCCAGAG 2785
Qy      3047  AACAAATAAAGAGGAGACAG 3068
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RESULT 2
BI488476 603020977F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191770 5',
LOCUS mRNA sequence.
DEFINITION BI488476.1 GI:153277704
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 786)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11479 row: i column: 19
High quality sequence stop: 781.
Location/Qualifiers
    1..786
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    /clone="IMAGE:5191770"
    /lab_host="DH10B"
    /clone_lib="NIH_MGC_114"
    /note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;
    Site:2: EcoRV (destroyed); RNA source anonymous pool of 6
    male brains, age range 23-27 yo. Library is oligo-dT
    primed and directionally cloned (EcoRV site is destroyed
    upon cloning). Average insert size 1.5 kb, insert size
    range 1-3 kb. Library is normalized and enriched for
    full-length clones and was constructed by C. Gruber
    (Invitrogen). Research Genetics tracking code 019. Note:
    this is a NIH_MGC Library."
BASE COUNT 192 a 223 c 205 g 166 t

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## ORIGIN

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Query Match 23.7%; Score 734; DB 12; Length 786;
Best Local Similarity 99.0%; Pred. No. 3.4e-93;
Matches 770; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

Qy      973  GCAGGATGATGAGATGAACATTTTCATCAACCTCACCAAGGATGATGTTGTAGAACTCCG 1032
Db      1  GCAGGATGATGAGATGAACATTTTCATCAACCTCACCAAGGATGATGTTGTAGAACTCCG 60
Qy      1033  AGCCCTGTGTCATTTGAGATGGTGTGGCCACAGACATGTCCTGCCATTTTCCAGCAAGTAAA 1092
Db      61  AGCCCTGTGTCATTTGAGATGGTGTGGCCACAGACATGTCCTGCCATTTTCCAGCAAGTAAA 120
Qy      1093  GACCATGAAGACAGACCTTTGCAACAGCTGGAGAGGATTGACAAGCCCAAGGCGCTCTCT 1152
Db      121  GACCATGAAGACAGACCTTTGCAACAGCTGGAGAGGATTGACAAGCCCAAGGCGCTCTCT 180
Qy      1153  ACTGCTCCATGCTGCTGACATCAGCCACCAACCAAGCAGTGGTGGTCCACAGCGCTTG 1212
Db      181  ACTGCTCCATGCTGCTGACATCAGCCACCAACCAAGCAGTGGTGGTCCACAGCGCTTG 240
Qy      1213  GACCAAGGCCCTCATGAGGAGGATTTCTCCGTCAGGCTCACAAAGGAGCAGAGTTGGCGCT 1272
Db      241  GACCAAGGCCCTCATGAGGAGGATTTCTCCGTCAGGCTCACAAAGGAGCAGAGTTGGCGCT 300
Qy      1273  GCCCTTTCTCCACTCTGTGACCCGACTTCCACTCTAGTGGCAGACAGTCTCAGATAGGTT 1332
Db      301  GCCCTTTCTCCACTCTGTGACCCGACTTCCACTCTAGTGGCAGACAGTCTCAGATAGGTT 360
Qy      1333  CATGCACTTCATTTGGAGGCCACATCTCTGCTGACTGACGTCAGGAGCAGAGAGTGT 1392
Db      361  CATGCACTTCATTTGGAGGCCACATCTCTGCTGACTGACGTCAGGAGCAGAGAGTGT 420
Qy      1393  TCAGCCCTGGCGGATGAGGACTCCAACTCTAAAACCAAGCCAGCTTTCAGTGGCGCA 1452
Db      421  TCAGCCCTGGCGGATGAGGACTCCAACTCTAAAACCAAGCCAGCTTTCAGTGGCGCA 480
Qy      1453  GCCCTCTCTGATGGAAGTGGGAGACCCCAACCTCATGTGTCAGCTTTCGTTCCAC 1512
Db      481  GCCCTCTCTGATGGAAGTGGGAGACCCCAACCTCATGTGTCAGCTTTCGTTCCAC 540
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Db      541  CTGGGTCAAGCGCATTCAGGAGATAACAGAAATGGAAGAACGGGAGCAAGTGGCAT 600
Qy      1573  CACCAACAGATGTCATTCAGAGCTGTCCCTCTGTGAAGAGAGGCCGCCATCCCC 1632
Db      601  CACCAACAGATGTCATTCAGAGCTGTCCCTCTGTGAAGAGAGGCCGCCATCCCC 660
Qy      163  TCCGGAAGATGAACAAACAGATGGGAATCTGGATTAGCCCTGGGCTGG-CCTAGGT 1691
Db      661  TCCGGAAGATGAACAAACAGATGGGAATCTGGATTAGCCCTGGGCTGGGCTGGCCAGGT 719
Qy      1692  CTTTCATTG-AGTCCAAAGTGTGATGTGTCATCAGCACCATCCATCAGGACTGGGTCCC 1748
Db      720  CTTTCATTGAGTCCAAAGTGTGATGTGTCATCAGCACCATCCATCAGGACTGGTCCCC 777

RESULT 3
BI390932 602417604F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4537009 5',
LOCUS mRNA sequence.
DEFINITION BI390932.1 GI:13284380
ACCESSION BI390932
VERSION BI390932.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 878)
NIH-MGC http://mgc.nci.nih.gov/.

```



TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
plate: LLAM10461 row: h column: 02  
High quality sequence stop: 688.  
Location/Qualifiers  
1. .878  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:4537009"  
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/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_92"  
/note="Organ: testis; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC library."  
BASE COUNT 202 a 232 c 256 g 188 t  
ORIGIN  
Query Match 21.5%; Score 665.2; DB 10; Length 878;  
Best Local Similarity 96.5%; Pred. No. 1.3e-83;  
Matches 745; Conservative 0; Mismatches 18; Indels 9; Gaps 6;  
QY 33 GGGCCAAAGAGGAAGTTGCCCTCTTGGGGCCCTGGGGCTCC- GGGGTGAGGATTTT 91  
DB 10 GGGCCAAAGAGGAAGTTGCCCTCTTGGGGCCCTGGGGCTCC- GGGGTGAGGATTTT 69  
QY 92 GATACCTGAGCAGGAACTTTGATCCCATGCCAAACCCCTGTTCTCTTCAGAGGAGC 151  
DB 70 GATACCTGAGCAGGAACTTTGATCCCATGCCAAACCCCTGTTCTCTTCAGAGGAGC 129  
QY 152 CACCTCCAGGGCCCATTTCTCAGGCTGGCTACATGGTGAACAGTTCGAGAGTGGGAG 211  
DB 130 CACCTCCAGGGCCCATTTCTCAGGCTGGCTACATGGTGAACAGTTCGAGAGTGGGAG 189  
QY 212 ATAAACATGAGGAGCTGAAGAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTC 271  
DB 190 ATAAACATGAGGAGCTGAAGAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTC 249  
QY 272 TACATAGATGAGACAGCGCAATCTTGGACAGGAGGAGAGCTGCAGAGCTGCGGTCA 331  
DB 250 TACATAGATGAGACAGCGCAATCTTGGACAGGAGGAGAGCTGCAGAGCTGCGGTCA 309  
QY 332 GATGCGCTCCCTTCGGAGTGGCGGACTGGCTGGCTCCACCTTCACCCAGCAGGCCGG 391  
DB 310 GATGCGCTCCCTTCGGAGTGGCGGACTGGCTGGCTCCACCTTCACCCAGCAGGCCGG 369  
QY 392 GCCAAGGCGCGGAGCAGAGAGAGCCCAAGTTCGGAAGCATTTGTGCACGCTGTGCAG 451  
DB 370 GCCAAGGCGCGGAGCAGAGAGAGCCCAAGTTCGGAAGCATTTGTGCACGCTGTGCAG 429  
QY 452 GCTGGGATCTTCGTGGAAGCGGATGTTCCGGAGAACATACACCTCTGTGGGCCCC- ACITTA 510  
DB 430 GCTGGGATCTTCGTGGAAGCGGATGTTCCGGAGAACATACACCTCTGTGGGCCCCAACITTA 489  
QY 511 CTCCTACTGGGTTCTCACTGCTCAAGAACCTGATCTCTGGTGGCTTTGATGCTTTTC 570  
DB 490 CTCCTACTGGGTTCTCACTGCTCAAGAACCTGATCTCTGGTGGCTTTGATGCTTTTC 549  
QY 571 CTTGAACAGGAGCAGATGACCATGCGCTGAGGACCATTTGTTTGTAGTTCTGACTCG 630  
DB 550 CTTGAACAGGAGCAGATGACCATGCGCTGAGGACCATTTGTTTGTAGTTCTGACTCG 609

QY 631 GCATACCTCATCAGCCGCTTCAAGATTCCTCCACTGTGTTTGTGATGAGTTTCTCTGATGC 690  
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QY 691 CTTGAGAGCAGG--CTATGGGAAGTACAGAATCTTACCAACAACAGATCCAGC--CA 745  
DB 668 CTTGAGAGCAGGCTATGGGAAGTACAGAATCTTACCAACAACAGATCCAGC--CA 727  
QY 746 GCGGATGTTACCCAGACAGTCCATGCTTCTTGTCTCCGACAGGATGATGTC 797  
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RESULT 4  
BQ179638 749 bp mRNA linear EST 30-APR-2002  
LOCUS UI-M-EVO-bws-e-08-0-UI.r1 NIH.BMAP\_EVO Mus musculus cDNA clone  
DEFINITION IMAGE:5701231 5', mRNA sequence.  
ACCESSION BQ179638  
VERSION BQ179638.1 GI:20355130  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)  
Seq primer: pYX-5 Location/Qualifiers  
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/dev\_stage="embryo 15.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH\_BMAP\_EVO"  
/note="Organ: brain; Vector: pYX-Asc; Site\_1: EcoR I; Site\_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fractionation, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTCGCTGGA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."  
BASE COUNT 183 a 207 c 181 g 178 t  
ORIGIN  
Query Match 20.8%; Score 643.4; DB 13; Length 749;  
Best Local Similarity 91.2%; Pred. No. 1.5e-80;

Matches 683; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 570 CCTTGACCGGAGGAGGATGACCATGCTGAGGACCATGTTTGGATGCTGACTC 629  
Db 1 CCTTGAACGGGAGCGATGACCATGCTGAGGACCATGTTTGGATGCTGACTC 60  
QY 630 GGCATACCTCATCAGCGGCTTCAAGATTCCTGACTGTTTGGATGCTGACTG 689  
Db 61 GGCATAGCCTCATCAGCGGCTTCAAGATTCCTGACTGTTTGGATGCTGACTG 120  
QY 690 CCTTGGAGAGGCTATGGAAGTACAAAGATCCTTACCACAAACAGATCCAGCGCG 749  
Db 121 CCTTGGAGAGGCTATGGAAGTACAAAGATCCTTACCACAAACAGATCCAGCGCG 180  
QY 750 ATGTTACCCAGACAGTCCATGCTTCTGCTCGCAGGATGGTGCATGCTGCTGCG 809  
Db 181 ACCTGACCCAGAGCTGCTTCTGCTCGCAGGATGGTGCATGCTGCTGCG 240  
QY 810 AGATTGAGCTTCTGCGGACATCATCTTGTGCTGAGTATCCATGATGAGCAGCGCA 869  
Db 241 AGATTGAGCTTCTGCGGACATCATCTTGTGCTGAGTATCCATGATGAGCAGCGCA 300  
QY 870 CTACCAACAGCTTCCACATCCAGACCAAGTCAAGATGTCATGCTGTAATGATCGTT 929  
Db 301 CAACCAACAGCTTCCACATCCAGACCAAGTCAAGATGTCATGCTGTAATGATCGAT 360  
QY 930 CAGTGTGGAGATCACCACATCAGCTCTGTTTCCGATGATGAGGATGATGATGA 989  
Db 361 CGGTGTGGAGATCACCACATCAGCTCTGTTTCCGATGATGAGGATGATGATGA 420  
QY 990 ACATTTTTCATCAACCTCACCAGGATGATGTTTGTGAGAACCTCCGCTGCTATGAGA 1049  
Db 421 ACATTTTTCATCAACCTCACCAGGATGATGTTTGTGAGAACCTCCGCTGCTATGAGA 480  
QY 1050 TGTGTGTGGCCAGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1109  
Db 481 TGTGTGTGGCCAGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
QY 1110 TGCACAGCTGGAGATGACAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1169  
Db 541 TGCACAGCTGGAGATGACAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
QY 1170 ACATCAGCACCACCAAGCAGTGGTGTGCTCAGAGCGCTTGGACCAAGGCGCTCATGG 1229  
Db 601 ACATCAGCACCACCAAGCAGTGGTGTGCTCAGAGCGCTTGGACCAAGGCGCTCATGG 660  
QY 1230 AGGAATTCCTCCTGAGGTGACAGAGGAGCAGATGGGCGCTGCTGCTGCTGCTGCTGCT 1289  
Db 661 AGAGATTCCTCCTCCTGAGGTGACAGAGGAGCAGATGGGCGCTGCTGCTGCTGCTGCTGCT 720  
QY 1290 GTACCCGCACTTCCACTCTAGTGGCAGAG 1318  
Db 721 GTATGCGCACTTCCACATGTTGGCCAG 749

RESULT 5  
BQ179626  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BQ179626 737 bp mRNA linear EST 30-APR-2002  
UI-M-EV0-bws-c-06-0-01.r1 NIH\_BMAP\_EV0 Mus musculus CDNA clone  
IMAGE:5701181 5', mRNA sequence.  
BQ179626  
BQ179626.1 GI:20355118  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NIH-MGC <http://mgc.nhl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cyabps-re@mail.nih.gov](mailto:cyabps-re@mail.nih.gov)

Tissue Procurement: Dr. James Lin, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: pYX-5.  
Location/Qualifiers  
1. 737  
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/lab\_host="embryo 15.5 dpc"  
/is\_lib="NIH\_BMAP\_EV0"  
/note="Organ: brain; Vector: pYX-Asc; Site: 1; Ecor I;  
Site: 2; Not I; The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured mRNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was size selected according to mRNA size fraction.  
ligated with Ecor I adaptor, digested with Not I, and then  
cloned directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is GTGCGTGGAA. This library was created for the  
University of Iowa Mouse Brain Molecular Anatomy Project  
(BMAP). Gene Discovery in the Developing Mouse Nervous  
System, supported by National Institutes of Mental Health  
(NIMH), Hsin-Chin, Ph.D., program coordinator."

BASE COUNT 182 a 204 c 176 g 175 t  
ORIGIN

Query Match 20.8%; Score 636.8; DB 13; Length 737;  
Best Local Similarity 91.8%; Pred. No. 1.3e-79;  
Matches 674; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 570 CCTTGAACCGGAGGAGGATGACCATGCTGAGGACCATGTTTGGATGCTGACTC 629  
Db 1 CCTTGAACCGGAGGAGGATGACCATGCTGAGGACCATGTTTGGATGCTGACTC 60  
QY 630 GGCATACCTCATCAGCGGCTTCAAGATTCCTGACTGTTTGGATGCTGACTG 689  
Db 61 GGCATAGCCTCATCAGCGGCTTCAAGATTCCTGACTGTTTGGATGCTGACTG 120  
QY 690 CCTTGGAGAGGCTATGGAAGTACAAAGATCCTTACCACAAACAGATCCAGCGCG 749  
Db 121 CCTTGGAGAGGCTATGGAAGTACAAAGATCCTTACCACAAACAGATCCAGCGCG 180  
QY 750 ATGTTACCCAGACAGTCCATGCTTCTGCTCGCAGGATGGTGCATGCTGCTGCG 809  
Db 181 ACCTGACCCAGAGCTGCTTCTGCTCGCAGGATGGTGCATGCTGCTGCG 240  
QY 810 AGATTGAGCTTCTGCGGACATCATCTTGTGCTGAGTATCCATGATGAGCAGCGCA 869  
Db 241 AGATTGAGCTTCTGCGGACATCATCTTGTGCTGAGTATCCATGATGAGCAGCGCA 300  
QY 870 CTACCAACAGCTTCCACATCCAGACCAAGTCAAGATGTCATGCTGTAATGATCGTT 929  
Db 301 CAACCAACAGCTTCCACATCCAGACCAAGTCAAGATGTCATGCTGTAATGATCGAT 360  
QY 930 CAGTGTGGAGATCACCACATCAGCTCTGTTTCCGATGATGAGGATGATGATGA 989  
Db 361 CGGTGTGGAGATCACCACATCAGCTCTGTTTCCGATGATGAGGATGATGATGA 420  
QY 990 ACATTTTTCATCAACCTCACCAGGATGATGTTTGTGAGAACCTCCGCTGCTATGAGA 1049  
Db 421 ACATTTTTCATCAACCTCACCAGGATGATGTTTGTGAGAACCTCCGCTGCTATGAGA 480







Db 564 GAAGTGGTTACAGCAAGCAAAAAATCCTTACCATAAOCATGATGCATGCAGCTGACGTC 623  
QY 755 ACCAGACAGCTCCATTCTTCCTCCGCGACAGGAGTGCTGACCTGCTGCGAGATT 814  
Db 624 ACACAGACTGTGATTACCTCTTTTATAAGACAGAGTAGCAAACTGGCTGACAGAGCTG 683  
QY 815 GAGCTCTGCGCATCATCTTGTGCTGAGCTATCCATGATTATGAGCACAGCGGCATACC 874  
Db 684 GAGATCTTTCAATAATCTTTTCGGCTGCCATCCATGACTATGAACATACTGGAACATCA 743  
QY 875 AACAGCTTCCACATCCAGCAAGTCCAGATGTCGATGTCGATGTCGATGTCGATGTCGATG 934  
Db 744 AACATTTCCACATCCAGCTCGTGCATGTCGATGTCGATGTCGATGTCGATGTCGATG 903  
QY 935 CTGAGAACACACATCAGCTCTCTTTCCGATTCATGACG---CATGATGAGATGAC 991  
Db 804 CTGAGAACACACATCAGCTCTCTTTCCGATTCATGACG---CATGATGAGATGAC 863  
QY 992 ATTTTCATCACTCCACCAAGATGAGTTGTGAGACCTCGGACCTGTCATGATGAGTG 1051  
Db 864 ATTTTCATCACTCCACCAAGATGAGTTGTGAGACCTCGGACCTGTCATGATGAGTG 923  
QY 1052 GTGTTGGCCACAGATGCTGCTCCATTTCCAGCAAGTGAAGACCATGAGACGCTTG 1111  
Db 924 GTATGGCCACAGATGCTGCTCCATTTCCAGCAAGTGAAGACCATGAGACGCTTG 983  
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Db 984 CAGCAACCAAGCAATTTGAGAACCCGAAAGCCCTTATCCCTCATGTACACACAGCAGAC 1043  
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Db 1104 GAGTCTTTAGACAGGCTGACAGAGAGGAGGAGTGGGCTGCGCTTTCTCCACATCTCT 1163  
QY 1292 GACCGCATCTTCACTCTAGTGGCACAGTCTCAGATAGGTTTCATGACATTCATGAGGAG 1351  
Db 1164 GACAGAAAGTCAACCATGTTGCTCAGTCACAGTGGTTTATTGACATTCATGAGGAG 1223  
QY 1352 CCCACATCTCTGCTGCTGACGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1411  
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QY 1412 GACTCCAGTCT 1423  
Db 1284 AGCTCCAGACT 1295

RESULT 8  
AK015375  
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DEFINITION  
AK015375 2128 bp mRNA linear HTC 05-DEC-2002  
Mus musculus adult male testis cDNA, RIKEN full-length enriched  
library, clone:493044A08 product:phosphodiesterase 1C, full insert  
sequence.  
ACCESSION  
VERSION AK015375.1 GI:12853690  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE  
1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 9279253  
PUBMED 10345636  
REFERENCE  
2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159  
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384 format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861  
4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,  
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I.,  
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,  
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Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
Hofmann, L., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,  
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Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,  
Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,  
Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.  
and Hayashizaki, Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
21085660  
11217851  
5

The FANTOM Consortium and the RIKEN Genome Exploration Research  
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Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2128)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,  
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,  
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,  
Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,  
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Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,  
Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission  
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
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Kanagawa 230-0045, Japan (E-mail: genome.res@gsr.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken

COMMENT

RESULT 9	
AK050499	
LOCUS	3451 bp mRNA linear HTC 05-DEC-2002
DEFINITION	Mus musculus adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820004L24 product:phosphodiesterase 1C, full insert sequence.
ACCSSION	AK050499
VERSION	AK050499.1 GI:26093967
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
REFERENCE	1
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)









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DEFINITION enriched library, clone: C230018D24 product: phosphodiesterase 1C,
full insert sequence.
ACCESSION AK082180
VERSION AK082180.1 GI:26349582
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SOURCE Mus musculus
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REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 9279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes

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Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:<http://genome.gsc.riken.go.jp/>  
URL:<http://fantom.gsc.riken.go.jp/>.

## FEATURES

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1258	Db	1258	GTGCTCAGTCACAAAGTGGGTTTATTGACTTCAATTTGTGGAGCCACCTTCTCTGTCTC	1317
1370	QY	1370	ACTGACGTGGCAGAGAAGTGTTCAGCCCTGCGGATGAGGACTCCAAGTCT	1423
1318	Db	1318	ACGGACATGACCGAGAAGATTGTGAGTCCATTAATGACGAAAGCTCCAGACT	1371
RESULT 14				
AK043647				
LOCUS	AK043647	4273 bp	mrna	linear HTC 05-DEC-2002
DEFINITION	Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830015G03 product:phosphodiesterase 1A, calmodulin-dependent, full insert sequence.			
ACCESSION	AK043647			
VERSION	AK043647.1	GI:26335810		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
1				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
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AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
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Direct Submission				
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.				
Please visit our web site for further details.				
URL: http://genome.gsc.riken.go.jp/				
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Location/Qualifiers				
1. .4273				









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